

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 174856

TO: Chun Crowder

Location: rem/3B59/3C70

Art Unit: 1644

Wednesday, December 28, 2005 Case Serial Number: 10/780043 From: Kristine Hensle

Location: Biotech-Chem Library

REM-1B69

Phone: (571) 272-4161

Kristine. Hensle@uspto.gov

Search Notes

Examiner Crowder,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Kristine Hensle Librarian STIC Biotech/Chem Library (571)272-4161



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mus musculu mus musculu tetraodon n brachydanio trypanosoma trypanosoma homo sapien fugu rubrip rubrip

05w431 05w436 05w435 06w435 06w435 04w45 07yuq1 07yuq3 06p2j1 06p2j1 096866 096866

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GO; GO:0005887; C:integral to plasma membrane; NAS.
GO; GO:000515; F:protein binding; IPI.
GO; GO:000717; P:protein binding; IPI.
InterPro; IPR007159; Ig.
InterPro; IPR00710; Ig-like.
SWART; SM00409; IG. II.
PROSTIE; PSS0835; IG. LIKE; I.
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Mammalia, Euthería, Buarchontoglires, Primates, Catarrhini, Hominidae,
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2006 (TrEMBLrel. 29, Last annotation update)
Activating receptor PILRbeta (Hypothetical protein DKFZp4340079)
Name=DKFZp4340079;
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98.2%; Pred. No. 5.6e-98;
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Listing first 45 summaries
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Post-processing:

Database

Result

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Minimum DB Maximum DB

Perfect score:

Sequence:

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Run on:

Scoring table:

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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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QBBYA6;
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MODERGER D. D., Banville D., L'Abbe D., Bouchard P., Shen S.H.;

"PILRalpha, a novel immunoreceptor tyrosine-based inhibitory motif-
bearing protein, recruits SHP-1 upon tyrosine-based inhibitory motif-
paired with the truncated counterpart PILRbeta.";

D. Biol. Chem. 275:4467-447(2000).

BMBL; AP161080; AAD52964.1; -; mRNA.

EMBL; AP161080; AAD52964.1; -; mRNA.

ROGO000088519; PILRA.

OO, GO:0005887; C:integral to plasma membrane; ISS.

GO; GO:0005115; P:protein binding; ISS.

ROGO000171; P:transmembrane receptor protein tyrosine kin. ..; ISS.

InterPro; IPR007110; Ig-like.
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                                                   121 SVYFCRVELDTRRSGRQQLQSIKGTKLTITQAVTTTTTWRPSSTTTIAGLRVTESKGHSE 180
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61 LAIVPNVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQESGFLRISNLRKEDQ 120
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81.9%; Score 973.5; DB 2; Length 303; 82.5%; Pred. No. 1.9e-80;
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                                                                                                                          181 SWHLSLDTAIRVALAVAVLKTVILGLLCLLLLWWRRRKGSRAPSSDF 227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunoglobulin domain; Receptor.
SEQUENCE 303 AA; 33878 MW; 0410ADFC7E80928B CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Inhibitory receptor FILRalpha.
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QBNH11;
01-OCT-2002 (TrEMBLrel. 2:
01-OCT-2002 (TrEMBLrel. 2:
                                                                                                                                                                                                                          QOUKJI HUMAN PRELIMINARY,
QOUKJI;
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MEDLINE=238825; PubMed=1247932; DOI=10.1073/pnas.242603899;
X MEDLINE=238825; PubMed=1247932; DOI=10.1073/pnas.242603899;
X Klausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Joedan H., Moore T., Max S.I., Wang J., Heish F.,
Altschul S.P., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
A stabledow L., Marusina K., Paramer A.A., Rubin G.M., Heish F.,
A stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A Raha S.S., Loquellano M.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,
Yillalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Mitching M., Madan A., Young A.C., Schwutz J., Myers R.M.,
Blakesley R.W., Touchman J.W., Garen B.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
M. Schnerch A., Schein J.E., Jones B.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human
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Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalla, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched
library, clone:A630007P20 product:weakly similar to INHIBITORY
RRCEPFOR PLIAALPHA.
Mame=Pilra; Synonym=AV021745;
Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.; Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases. EMBL, BC077812; AAH17812.1; -; mRNA. InterPro; IPR003599; IG. InterPro; IPR007110; IG-11ke.
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SEQUENCE 226 AA; 25479 MW; 5938181797733A30 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Last sequence update)

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Sequence 6, Appli
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1 MGRPLLLPLLLLLQPPAFLQ......LCLLLWWRRKGSRAPSSDF 226
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/cgn2_6/ptodata/1/iaa/6_COMB.pep:*
/cgn2_6/ptodata/1/iaa/H_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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-09-869-388-6
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Sequence 22, Appl Sequence 5, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 10, Appli Sequence 21, Appl Sequence 213, App Sequence 213, App	AND RELATED COMPOSITIONS A	COTE 1189; DB 2; Length 226; red. No. 1.4e-107; Mismatches 0; Indels 0; Gaps 0; GSTGSGPSYLYGVTQPKHLSASMGGSVEIPPSFYYPWE 60 GSTGSGPSYLYGVTQPKHLSASMGGSVEIPPSFYYPWE 60 STRPPSIHKDYVNRLFLNWTEGGESGFLRISNLRKEDQ 120 STRPPSIHKDYVNRLFLNWTEGGESGFLRISNLRKEDQ 120 STRPPSIHKDYVNRLFLNWTEGGESGFLRISNLRKEDQ 120 KGTKLTITQAVTTTTTWRPSSTTTIAGLRVTESKGHSE 180 KGTKLTITQAVTTTTTWRPSSTTTIAGLRVTESKGHSE 180 ILIGHLCLLLWWRRRKGSRAPSSDF 226 ILIGHLCLLLWWRRRKGSRAPSSDF 226 ILIGHLCLLLWWRRRKGSRAPSSDF 226
US-09-778-510-22 US-10-630-406-5 US-08-559-628-5 US-08-56-164A-2 US-08-653-4028-2 US-08-653-4028-2 US-09-661-052-4 US-09-108-08-4 US-09-102-716-4 US-09-102-716-4 US-09-102-716-4 US-09-102-716-4 US-09-102-716-4 US-09-102-716-28 US-09-102-716-28 US-09-907-754-213 US-09-906-700-213 US-09-906-700-213 US-09-906-700-213	ALIGNMENTS 9869388 1e -DERIVED NUCLEIC ACIDS US/09/869,388	imilarity 100.0%; Pred. No. 1.4e-107; Conservative 0; Mismatches 0; Indels MGRPLLDLLLLOPPAFLQPGSTGSGPSYLYGVTQPKHLSASMGGAFLINTLLLLQPPAFLQPGSTGSGPSYLYGVTQPKHLSASMGGAFLINTLLLLQPPAFLQPGSTGSGPSYLYGVTQPKHLSASMGGAFLINTLLLLQPPAFLQPGSTGSGPSYLYGVTQPKHLSASMGGAFTATAPPRISTREASMGGAFTATTAPPREASMGGAFTATTAPPREASMGGAFTATTAPPREASMGGAFTATTAPPREASMGGAFTATTAPPREATTAPPREATTAPPREATTAPPREATTATTAPPREA
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	ALIGORATE TO SECULT 1 US-09-869-388-10 US-09-869-388-10 Sequence 10, Application US/09869388 Patent No. 6774214 GENERAL INFORMATION: APPLICANT: Bates, Elizabeth APPLICANT: Fournier, Nathalie APPLICANT: Fournier, Nathalie APPLICANT: GABLE, Lidoel TITLE OF INVENTION: MONOCYTE-DERIVED FILE REFERENCE: SF0977X CURRENT APPLICATION NUMBER: US/09/86; CURRENT FILING DATE: 2002-02-21 NUMBER OF SEQ ID NOS: 14 SOFTWARE: IBM PC compatible SOFTWARE: IBM PC compatible SOFTWARE: IBM PC compatible TENGTH: 226 TYPE: PT ORGANISM: homo sapiens	Similarity 100.0%; Score 11 Similarity 100.0%; Pred. No 6; Conservative 0; Mismat. MGRPLLLPLLLLQPPAPLQPGSTGSGP IMTERIATE OF STATES O
	-10 6774214 6774214 6774214 6774214 Chalus Chalus Garron NVENTION NVENTION NVENTION SEC ID N LING DAT	νω 1 ν Ο
100 102 103 103 104 101 101 101 101 100 100 100 100 100	ULT 1 Gquence 10, Applatent No. 6774 SHEEL NO. 6774 SHEEL NO. 6774 SHEELCANT: BAPLICANT: CAPPLICANT: CAPPLICANTS TO 10 LENGTH: 226 TYPE: PAT CAPPLICANT: 236 TYPE: CAPPLICANT: 2	uery Match est Local S atches 226 1 1 1 121 121 121 121 121 121 209-869-388- equence 6, atent No. 6 atent No. 6 APPLICANT: APPLICANT: APPLICANT:
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R PILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,581

R PILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,584

R PILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,500

R R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,500
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R APPLICATION NUMBER: 60/047,492
R PILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,598
R PILING DATE: 1997-05-23
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R APPLICATION NUMBER: 60/043,312
R FILING DATE: 1997-04-11
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R APPLICATION NUMBER: 60/043,672
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,596
APPLICATION NUMBER: 60/047,612
APPLICATION NUMBER: 60/047,612
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FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,568
FILING DATE: 1997-04-11
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FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,311
FILING DATE: 1997-04-11
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FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,669
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APPLICATION NUMBER: 60/056,889
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APPLICATION NUMBER: 60/056,630
                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/047,618
FILING DATE: 1997-05-23
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,592
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APPLICATION NUMBER: 60/047,632
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APPLICATION NUMBER: 60/047,601
FILING DATE: 1997-05-23
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FILING DATE: 1997-04-11
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APPLICATION NUMBER: 60/056,886
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FILING DATE: 1997-08-22
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APPLICATION NUMBER: 60/
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APPLICATION NUMBER: 60
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UB-10-780

"TILE OF INVENTION: MONOCYTE-DERIVED NUCLEIC ACIDS AND RELATED COMPOSITIONS AND METHO
FILE REPERENCE: 8F0977X
CURRENT APPLICATION: 2002-02-21
NUMBER OF SEQ ID NOS: 14
SOPTWARE: IBM PC compatible
SOPTWARE: IBM PC compatible
LENGTH: 27
TYPE: pp...
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97.9%; Score 1163.5; DB 2
Best Local Similarity 98.2%; Pred. No. 4.1e-105;
Matches 223; Conservative 1; Mismatches 2;
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TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: PZ002P1
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CURRENT PELING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: US/09/149,476
CURRENT FILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER PILING DATE: 1997-03-07
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EARLIER PELING DATE: 1997-03-07
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EARLIER PILING DATE: 1997-05-23
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R APPLICATION NUMBER: 60/047,615

R APPLICATION NUMBER: 60/047,597

R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,597

R FILING DATE: 1997-05-23

R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,603
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APPLICATION NUMBER: 60/047,583
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APPLICATION NUMBER: 60/047,617
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Patent No. 6420526
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p ORGANISM: homo sapiens
US-09-869-388-6
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Sequence 2073, Application US/11054515
Publication No. US2005025532A1
Publication No. US2005025532A1
Publication No. US2005025532A1
APPLICANT: RUADEN OF al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REPERENCE: PF523P3
CURRENT PAPLICATION NUMBER: US/11/054,515
CURRENT PILING DATE: 2005-02-10
PRIOR APPLICATION NUMBER: 60/543,296
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2095, Ap
2095, Ap
897, Ap
1016, Ap
11131, Ap
1163, Ap
1184, Ap
1284, Ap
128
                                                                                                                               ; Search time 4.28252 Seconds (without alignments) 376.418 Million cell updates/sec
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(cgn2_6/ptodata/2/pubpaa/USO8 NEW PUB.pep:*

(cgn2_6/ptodata/2/pubpaa/USO7 NEW PUB.pep:*

(cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

(cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

(cgn2_6/ptodata/2/pubpaa/USO7 NEW_PUB.pep:*

(cgn2_6/ptodata/2/pubpaa/USO1 NEW_PUB.pep:*

(cgn2_6/ptodata/2/pubpaa/USO10 NEW_PUB.pep:*

(cgn2_6/ptodata/2/pubpaa/USO11 NEW_PUB.pep:*

(cgn2_6/ptodata/2/pubpaa/USO11 NEW_PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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US-11-054-515-2073

US-11-054-515-907

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US-11-054-515-1163
US-11-054-515-1893
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                                                                                                                               December 23, 2005, 20:41:30
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Maximum Match 100%
Listing first 45 summaries
                                                                                     - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46 GGSVEI-----PFSFYYPWELATAPDVRISWRRGHF---HGQSFYSTRPPSIHKDYVN 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15 GSSVKVSCKASGGTFSSYALSWVRQAPGQGLEW-MGIFIPIFGTEYYAER-----FPG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126 GSGGGGGGGGAGASAQAVLT----QPSSVSGAPQQRVTISCTGSSSNIGAGYDVHWYQQL 179
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#FILE REFERENCE: PF523P3
CURRENT APPLICATION NUMBER: US/11/054,515
CURRENT PILING DATE: 2005-02-10
PRIOR APPLICATION NUMBER: 60/543,296
PRIOR PILING DATE: 2004-02-11
PRIOR PILING DATE: 2004-02-11
PRIOR PLICATION NUMBER: 60/580,347
PRIOR PILING DATE: 2002-11-14
PRIOR PILING DATE: 2001-11-16
PRIOR PILING DATE: 2001-11-16
PRIOR PILING DATE: 2001-11-16
PRIOR PILING DATE: 2001-12-19
PRIOR PILING DATE: 2001-12-19
PRIOR PILING DATE: 2001-6-15
PRIOR PILING DATE: 2001-6-15
PRIOR PILING DATE: 2001-6-15
PRIOR PILING DATE: 2001-06-15
PRIOR PILING DATE: 2001-03-11
PRIOR PILING DATE: 2001-03-11
PRIOR PILING DATE: 2001-03-16
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PRIOR FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/580,347
PRIOR PILING DATE: 2004-06-18
PRIOR APPLICATION NUMBER: 10/293,418
PRIOR PILING DATE: 2002-11-14
PRIOR PILING DATE: 2001-11-16
PRIOR PILING DATE: 2001-11-16
PRIOR PILING DATE: 2001-12-19
PRIOR PILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/294,48
PRIOR PILING DATE: 2001-05-25
PRIOR PILING DATE: 2001-05-25
PRIOR PELING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
US-11-054-515-2073
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APPLICANT: Fraunhofer Gesellschaft zur F'rderung der angewandten Forschung e.V.
TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
TITLE OF INVENTION: Antibody fragments and fusions mediated plant disease
TITLE OF INVENTION: resistance against fungi
FILE REFERENCE: 3581.01US01
CURRENT APPLICATION NUMBER: US/10/512,184
CURRENT FILING DATE: 2044-10-22
NUMBER OF SEQ ID NOS: 72
SEQ ID NO 26
LENGTH: 258
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; APPLICANT: Praunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73 RGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQESG---FLRISNLRKEDQSVYFCRVEL 129
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                                                                                                                                                                                                                                                                                                                                                                                                                      78 GQS----FYS--TRPPSIHKDYVNRLFLNWTEGQESG---FLRISNLRKEDQSVYFCRVE 128
                                                                                                                                                                                                                                                                                                                                                                                     22 GGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWELATAPDV----RISWRRGHFH 77
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                                                                                                                                                                                                                                                                                                                              35; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43; Indels 36; Gaps
PRIOR FILING DATE: 2000-10-17
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 907
                                                                                                                                                                                                                                                                 9.3%; Score 110.5; DB 7; Length 256; 29.1%; Pred. No. 0.0011; tive 20; Mismatches 45; Indels 35
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--SSYAGRSTYVFGTGTKVTV 254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
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Best Local Similarity 29.1%
Matches 41, Conservative
                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
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US-10-512-184-62
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Sequence 106, App
Sequence 128, App
Sequence 6, Appli
Sequence 7, Appli
Sequence 21, Appli
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2, Appli
2, Appli
                                                                 December 23, 2005, 20:40:10 ; Search time 76.8906 Seconds (without alignments) 1228.101 Million cell updates/sec
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                                                                                                                                   1 MGRPLLLPLLLLLQPPAFLQ......LCLLLWWRRRKGSRAPSSDF 226
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5.1.6
Compugen Ltd
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US-10-450-763-33210
US-10-450-763-47228
US-10-450-763-51762
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US-10-262-445-128
US-10-80-043-6
US-10-820-474A-7
US-09-803-391-485
US-09-803-391-485
US-09-882-171-485
US-09-774-2380
US-09-882-171-485
US-09-774-381-58
US-10-164-861-485
US-10-29-631-2
US-10-790-043-2
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GenCore version (c) 1993 - 2005
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Maximum Match 100%
Listing first 45 summaries
                                            - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Perfect score:
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No.
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Sequence 711, App Sequence 4, Appli Sequence 4, Appli Sequence 8, Appli Sequence 92, Appli Sequence 174, App Sequence 116, Appl Sequence 11, Appli Sequence 11, Appli	TAP-1, AND PA-I MOLECULES
3 US-09-866-050A-711 4 US-10-290-631-4 4 US-10-777-524-4 5 US-10-777-521-4 5 US-10-770-073-8 6 US-10-788-625-92 4 US-10-479-670-174 4 US-10-479-670-168 4 US-10-270-073-6 4 US-10-28-917-11 4 US-10-28-917-11 4 US-10-28-917-11 4 US-10-28-917-11 4 US-10-28-917-11 4 US-10-28-917-11 4 US-10-28-917-11 4 US-10-33-448-11 4 US-10-378-567-2 4 US-10-378-567-2 4 US-10-270-071-184 5 US-10-270-071-184 6 US-10-270-071-184 7 US-10-270-071-184 8 US-10-270-071-184 8 US-10-270-071-184	MIR-1, LSP-1, REFOR 7774,381 354 674 149 347 159 159 143 414 571
377 31.7 224 226 19.0 99 226 19.0 99 226 19.0 99 122.5 10.2 257 121.5 10.2 253 121.5 10.2 255 115.5 9.7 310 115.5 9.7 448 115.5 9.7 448 114.5 9.6 261 114.5 9.6 261	1-381-44 10. 11
2000 0 1 2 2 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	RESULT 1 US-09-774-3 Sequence Sequence GENERAL II RESTICAN APPLICAN APPLICAN APPLICAN TITLE OF TITLE TITLE OF T

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Gaps

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Length 226; Indels

Query Match 100.0%; Score 1189; DB 3; Best Local Similarity 100.0%; Pred. No. 8.5e-99; Matches 226; Conservative 0; Mismatches 0;

1 MGRPLLLPLLLLLQPPAFLQPGGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE

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Sequence Sequence Sequence

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61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTBGQBSGFLRISNLRKEDQ 120
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                                                                                                                                                                          COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/745,763
FILING DATE: 18-Jun-2000
CLASSIPICATION: «UNKNOWN-
ATTORNEY/AGBNT INFORMATION:
NAME: Sprunger, Suzanne A.
REGISTRATION NUMBER: 41,323
TELEPHONE: (617) 898-284
TELEPHONE: (617) 876-581
INFORMATION POR SEQ ID NO: 106:
SEQUENCE CHARACTERISTICS:
INFORMATION POR SEQ ID NO: 106:
SEQUENCE CHARACTERISTICS:
JENGTH: 226 amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
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                    NUMBER OF SEQUENCES: 219
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 106:
US-09-745-763-106
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Publication No. US20040014058A1
GENERAL INFORMATION:
APPLICANT: Alsobrook II, John
APPLICANT: Burgess, Catherine
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Chant, John
Chaudhuri, Amitabha
Bdinger, Shlomit
Gerlach, Valerie
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Gorman, Linda
Guo, Xiaojia
Kekuda, Ramesh
Mezes, Peter
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APPLICANT:
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APPLICANT:
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APPLICANT:
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APPLICANT: Bates, Milabeth
APPLICANT: Betes, Libral
APPLICANT: Fournier, Nathalie
APPLICANT: Chalus, Libral
APPLICANT: Chalus, Libral
APPLICANT: Chalus, Libral
APPLICANT: Chalus, Libral
APPLICANT: Garrone, Pierre
TITLE OF INVENTION: MONOCYTE-DERIVED NUCLEIC ACIDS AND RELATED COMPOSITIONS AND METHC
CURRENT APPLICATION NUMBER: US/10/869,388
PRIOR PAPLICANTON NUMBER: US/09/869,388
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 10
LENGTH: 226
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                                                                                 61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTBGQESGFLRISNLRKEDO 120
                                                                                                                                                  SVYPCRVELDTRRSGRQQLQSIKGTKLTITQAVTTTTTWRPSSTTTTIAGLRVTESKGHSE 180
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1 MGRPLLLPLLLLLQPPAFLQPGGSTGSGPSYLYGVTQPKHLSASMGGSVBIPFSFYYPWE
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Treacy, Maurice
Spaulding, Vikki
Spaulding, Vikki
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 226;
                                                                                                                                                                                                                                                181 SWHLSLDTAIRVALAVAVLKTVILGILCILLIWWRRRKGSRAPSSDF 226
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100.0%; Pred. No. 8.5e-99;
tive 0; Mismatches 0;
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Patent No. US20020065394A1
GENERAL INFORMATION:
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# Publication No. US20040137506A1
# GENERAL INFORMATION:
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LaVallie, Edward R.
Collins-Racie, Liss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Jacobs, Kenneth
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Best Local Similarity 100.
Matches 226; Conservative
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ORGANISM: homo sapiens
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US-09-745-763-106
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December 23, 2005, 20:18:33 ; Search time 94.0207 Seconds (without alignments) 1056.147 Million cell updates/sec
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1189
1 MGRPLLLPLLLLLQPPAFLQ......LCLLLWWRRKKGSRAPSSDF 226
                                                                                                                                                                                                                                                                                                                                                                                  2443163
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                        2443163 segs, 439378781 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                          OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1: geneseqp1980s:*
2: geneseqp290s:*
4: geneseqp2000s:*
5: geneseqp2001s:*
6: geneseqp2001s:*
7: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2003bs:*
                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                      Perfect score:
                                                                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database :
                                                                                                                                                                                                                                       Sequence:
                                                                                                                                                                                                                                                                                                                                          Searched:
                                                                                                                    Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	uo.	Human LSP	A human m	A secrete	Human pol	A human m	TNF-recep	Human sec	Human sec	Human sig	Human nov	Region of	Novel hum	Human sec	Human imm	A human m	PRO polyp		Novel hum	Novel hum	Novel hum	Human imm	A human m	Human NOV	A human m
	Description	Aay08015	Aab07447	Aaw80407	Abp61825	Aab07445	Abu89824	Aaw63682	Abb12010	Aay87230	Abg95345	Abo34539	Ad123200	Adh74202	Aaw62772	Aab07443	Adp25129	Abg00509	Abg16869	Abg02851	Abg21403	Adk98565	Aab07444	Ade95578	Aab07446
SUMMARIES	QI QI	AAY08015	AAB07447	AAW80407	ABP61825	AAB07445	ABU89824	AAW63682	ABB12010	AAY87230	ABG95345	AB034539	ADI23200	ADH74202	AAW62772	AAB07443	ADP25129	ABG00509	ABG16869	ABG02851	ABG21403	ADK98565	AAB07444	ADE95578	AAB07446
	DB	~	m	7	Ŋ	m	9	N	4	m	S	9	7	œ	~	m	œ	4	4	4	4	œ	m	7	М
	Query Match Length DB	226	226	226	226	227	227	291	326	227	238	238	238	238	303	303	303	1012	1012	1012	1012	228	230	230	175
عد	Query Match	100.0	100.0	99.5	99.5	97.9	97.9	97.9	97.9	96.8	89.7	89.7	89.7	89.7	81.9	81.9	81.9	64.3	64.3	64.3	64.3	63.8	63.8	63.8	63.7
	Score	1189	1189	1183	1183	1163.5	1163.5	1163.5	1163.5	1150.5	1067	1067	1067	1067	973.5	973.5	973.5	765	765	765	765	759	759	759	757.5
	Result No.	н	8	m	4	Ŋ	9	7	ω	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24

Ade95580 Human NOV	Aaw75053 Fragment	Abg95614 Human nov		Adi23469 Novel hum	Adh74471 Human sec	Abb72387 Murine pr	Ade59537 Rat Prote		Abr42758 Anti-CEA	Aab19873 Activatin	Abu97134 Recombina	Abr42757 Anti-CEA	Aau72792 Human ant	Aab19871 Activatin	Abu97128 Recombina		Abb09605 Amino aci	Abg74386 Single ch		Ado40448 Human sin
7 ADE95580	2 AAW75053	5 ABG95614	6 ABO34808	7 ADI23469	8 ADH74471	5 ABB72387	7 ADE59537	~	y W	4 AAB19873	6 ABU97134	6 ABR42757	S	4 AAB19871	9	2 AAW83324	S ABB09605	6 ABG74386	7 ADG98739	8 ADO40448
50.3 206	44.9 101	44.9 101	44.9 101	44.9 101	44.9 101		31.1 212						10.2 271	9.8 555	9.8 252		9.7 310		9.7 310	9.7 310
25 598	26 534	27 534	28 534	29 534	30 534	31 377	32 369.5	33 226	34 122.5	35 122	36 121.5	37 121	38 121	39 116.5	40 116	41 115.5	42 115.5	43 115.5	44 115.5	45 115.5

ALIGNMENTS

RESULT 1

proliferin analogue I; thrombopoietin analogue protein-1; PA-1; TAP-1; cancer; proliferin analogue I; thrombopoietin analogue protein 1; anticancer; proliferation; differentiation; inflammatory; disease; growth; proliferation; differentiation; cell survival; angiogenesis; diagnosis; thrombopoiesis; prognosis; treatment; chromosome megakaryocytopoiesis; thrombopoiesis; thrombopoicsis; thrombopoicsis; thrombopoicsis; thrombopoicsis; bone mazrow transplant; infection; intravascular coagulation: iron deficiency; HIV; human. (MILL-) MILLENNIUM BIOTHERAPEUTICS INC. AAY08015 standard; protein; 226 AA. Pan Y, Gearing DP, Mccarthy SA; 97US-0061149P. 97US-0061159P. 98US-00004206. 98US-00010674. 97US-0061143P. 98WO-US021151 (first entry) Human LSP-1 protein. WPI; 1999-264042/22. N-PSDB; AAX37558; W09918243-A1.7 08-JUL-1999 15-APR-1999. Homo sapiens 06-OCT-1997; 06-OCT-1997; 06-OCT-1997; 06-OCT-1998; 08-JAN-1998; 22-JAN-1998; 27-JAN-1998; AAY08015; AAYOBO15

XX AAY

XX A

Signal-peptide containing proteins that modulate cellular processes.

Claim 2; Fig 1; 124pp; English.

This invention describes the isolation of nucleic acids encoding the

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proliferin analog I (PA-I) and thrombopoietin analog protein-1 (LSP-1).
These proteins have antianglogenic, anticancer, anti-inflammatory anti-
arthritic and anti-thrombopytopenic, anticancer, anti-inflammatory, anti-
arthritic and anti-thrombopytopenic activity. The products of the
inflammatory responses, growth, proliferation, differentiation and
curvival of cells, angiogenesis, maturation of haematopoietic stem cells
and erythroid precursors megakaryocytopoiesis and thrombopoiesis.
Antibodies, or other binding agents, specific for the products of the
Antibodies, or other binding agents, specific for the products of the
invention are useful for diagnosis, prognosis and monitoring of treatment
of diseases. Other uses include chromosome mapping, identification of
individuals (tissue typing) and in forensic studies. LSP-1, PA-I and TAP-
I proteins and nucleic acids are modulators of cellular processes,
particularly they are used to treat or prevent diseases associated with
deregulation of angiogenesis, immune responses and haematopoiesis, e.g.
cancer, arthritis (and other inflammatory diseases), thrombocytopenia
(caused by cancer treatment, bone marrow transplant, human immune
caused control of the cont
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 SVYPCRVELDTRRSGRQQLQSIKGTKLTITQAVTTTTTWRPSSTTTIAGLRVTESKGHSE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MGRPLLLPLLLLLQPPAFLQPGGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60
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FDF03-M14, FDF03-S2, haematopoietic cell, monocyte hyperplasia; 
tissue rejection, inflammation, infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 1189; DB 2; Length 226; 100.0%; Pred. No. 1.7e-95; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 SWHISLDTAIRVALAVAVLKTVILGELCILLWWRRRKGSRAPSSDF 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWHLSLDTAIRVALAVAVLKTVILGLLCLLLWWRRRKGSRAPSSDF 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A human monocyte-derived protein FDF03-S2.
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98US-00224604
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                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 226 AA;
                                                                                                                                                                                                                                                                                                                                                                     deficiency etc
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31-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-DEC-1999;
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The present sequence represents a human monocyte-derived protein. The specification describes monocyte-derived proteins FDF03-FDF03DeltaTM, FDF03-S1. FDF03-M14, and PDF03-S2. The proteins are involved in the requiation, or development, of haematopoietic cells. Antibodies specific for antigenic components of the proteins can be used to screen for components in samples. The proteins can also be used to screen for candidate therapeutic agents. The monocyte-derived proteins and polymucleotides can be used for diagnosis of diseases related to an increase, or decrease, in the number of monocytes in a tissue or lymph system, such as monocyte hyperplasia, tissue or graft rejection, inflammation, or bacterial or viral infections. The proteins can also be used in the treatment of disorders associated with abnormal expression or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQESGFLRISNLRKEDQ 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 SVYFCRVELDTRRSGRQQLQSIKGTKLTITQAVTTTTTWRPSSTTTIAGLRVTESKGHSE 180
                                                                                                                                                                                            Novel monocyte-derived polypeptides and polynucleotides, used to diagnose diseases associated with changes in monocyte numbers, e.g. bacterial or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQESGFLRISNLRKEDQ 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 1189; DB 3; Length 226; 100.0%; Pred. No. 1.7e-95; tive 0; Mismatches 0; Indels 0.
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                                                        Garrone P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A secreted protein encoded by clone di39_9.
                                                                                                                                                                                                                                                                                                                Claim 1; Page 41-42; 45pp; English.
                                                        Chaulus L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW80407 standard; protein; 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 226; Conservative
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                                                        Bates E, Fournier N,
(SCHE ) SCHERING CORP.
                                                                                                                 WPI; 2000-465984/40
                                                                                                                                                                                                                                                          viral infections.
                                                                                                                                               N-PSDB; AAA58818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 226 AA;
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13-JAN-1999
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December 23, 2005, 20:18:33 ; Search time 72.8036 Seconds (without alignments) 1056.147 Million cell updates/sec
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1 MGRPLLLPLLLPPAFLQ......KTQRSHMRISGMKDKIQIPS 175
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Compugen Ltd.
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GenCore version
Copyright (c) 1993 - 2005
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geneeqp2000s: 4
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		Aaw62772 Human imm		Adp25129 PRO polyp		Aab07444 A human m	Ade95578 Human NOV	Abg00509 Novel hum	Abg16869 Novel hum	Abg02851 Novel hum	Abg21403 Novel hum		Aay08015 Human LSP	Aab07447 A human m	p61825 Human pol	Abg95345 Human nov	034539 Region of	Adi23200 Novel hum	Adh74202 Human sec	Aab07445 A human m	Abu89824 TNF-recep	Aaw63682 Human sec	Abb12010 Human sec	Aay87230 Human sig
SUMMARIES	Dο	07446	AAW62772 Aa	e	ADP25129 Ad	ADK98565 Ad	AAB07444 Aa	ADE95578 Ad	ABG00509 Ab	ABG16869 Ab	ABG02851 Ab	ABG21403 Ab	AAW80407 Aa	AAY08015 Aa	AAB07447 Aa	ABP61825 Ab	ABG95345 Ab	ABO34539 Ab	AD123200 Ad	ADH74202 Ad	AAB07445 Aa	ABU89824 Ab	AAW63682 Aa	ABB12010 Ab	AAY87230 Aa
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•	Ouery Match	100.0	87.9	87.9	87.9	87.4	87.4	87.4	86.7	86.7	86.7	86.7	81.1	81.1	81.1	81.1	79.6	79.6	79.6	79.6	79.5	79.5	79.5	79.5	78.1
	Score	934	821	821	821	816	816	816	809.5	809.5	809.5	809.5	757.5	757.5	757.5	757.5	743.5	743.5	743.5	743.5	742.5	742.5	742.5	742.5	729.5
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Ade95580 Human NOV Aww75053 Fragment Ab034808 Fragment Adi23469 Novel hum Adh14471 Human sec Abb7236 Murine pr Ade59537 Rat Prote Aww5773 Partial m Abu97118 Recombina Abu97128 Recombina Abu97128 Recombina Abu97134 Recombina Abu97138 Recombina Abu97138 Recombina Ads09256 Human c-M Adg32317 Chicken s Adg32355 Precursor Adg32355 Precursor	
ADE95580 AAW75053 ABG95614 ABG95614 ABD723469 ADT23469 ADT234671 ABB72387 ADE55537 ABU97118 ABU97118 ABU97118 ABU97134 ADG32355 ADG32355	ADG32338 ABP46066
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ALIGNMENTS

RESULT 1

Human; monocyte-derived protein; FDF03; FDF03DeltaTM; FDF03-S1; FDF03-M14; FDF03-S2; haematopoietic cell; monocyte hyperplasia; tissue rejection; inflammation; infection. Garrone P; A human monocyte-derived protein FDF03-M14. 1. .17 /note= "signal sequence" 18. .175 /note= "mature protein" Location/Qualifiers AAB07446 standard; protein; 175 AA. Chaulus L, 99WO-US030004. 98US-00223919. 98US-00224604. (first entry) Bates E, Fournier N, (SCHE) SCHERING CORP. WO200040721-A1 20-OCT-2000 29-DEC-1999; 31-DEC-1998; 31-DEC-1998; Homo sapiens 13-JUL-2000 AAB07446; Protein Peptide Key AAB07446

WPI; 2000-465984/40. N-PSDB; AAA58817.

Novel monocyte-derived polypeptides and polynucleotides, used to diagnose diseases associated with changes in monocyte numbers, e.g. bacterial or viral infections.

Claim 1; Page 39-40; 45pp; English.

The present sequence represents a human monocyte-derived protein. The specification describes monocyte-derived proteins FDF03, FDF03DeltaTM, FDF03-S1, FDF03-M14, and FDF03-S2. The proteins are involved in the

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regulation, or development, of haematopoietic cells. Antibodies specific for antigenic components of the proteins can be used to detect the components in samples. The proteins can also be used to exceen for candidate therapeutic agents. The monocyte-derived proteins and polymucleotides can be used for diagnosis of diseases related to an increase, or decrease, in the number of monocytes in a tissue or lymph system, such as monocyte hyperplasia, tissue or graft rejection, inflammation, or bacterial or viral infections. The proteins can also be used in the treatment of disorders associated with abnormal expression or used in the components.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; type I transmembrane protein; immunoglobulin-like domain; FDF03; activated monocyte; YE01; KTE03; control; development; differentiation; mammalian immune system; treatment; cancerous condition; degenerative condition; autoimmune response; transplantation rejection; graft versus host disease; inflammatory condition; detection; diagnosis; drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGRPLLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 934; DB 3;
; Pred. No. 1.4e-80;
0; Mismatches 0;
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96US-00762187.
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                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 175; Conservative
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Lanier LL,
                                                                                                                                                                                                                                                                                               signalling by a monocyte
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                                                                                                                                                                                                                                                                                                                                                          Sequence 175 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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21-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9824906-A2
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09-DEC-1996;
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AAM62772
ID AAM62772
AAM 62772
AAM 6273
BDT 23-83
BDT 23-83
CXX Human
XXX Human
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transmembrane protein comprising an extracellular portion characterised by immunoglobulin-like domains, indicating that the protein is a receptor member of the immunoglobulin superfamily. The PDF03 gene is found in activated monocytes. The specification also describes other proteins encoded by activated monocytes, which are designated YE01 and KTE03. The genes function in controlling development, differentiation, and/or physiology of the mammalian immune system. The products can be used for treating abnormal proliferation, regeneration, degeneration or atrophy. They can be used for treating e.g. cancerous conditions, degenerative conditions, autoimmune responses, transplantation rejection, graft versus host disease, or inflammatory conditions. The products can also be used for detection, disagnosis and drug screening
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel monocyte-derived polypeptides and polynucleotides, used to diagnose
                                                                                                                                                                                                                                                                                                                                                                                   61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQ 120
                                                                                                                                                                                                                                                                                                                                                                                                   present sequence represents a human protein, FDP03, which is a type I
                                                                                                                                                                                                                                                                                                                                          1 MGRPLLLFPLLFPRAFLQPSGSTGSGPSYLYGYTQPKHLSASMGGSVEIPFSFYYFWE 60
                                                                                                                                                                                                                                                                                                                        1 MGRPLLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPXHLSASMGGSVEIPFSFYYPWE
                                                                                                                                                                                                                                                                                            Gape
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, monocyte-derived protein; FDF03; FDF03DeltaTM; FDF03-S1;
FDF03-M14; FDF03-S2; haematopoietic cell; monocyte hyperplasia;
tissue rejection; inflammation; infection.
                                                                                                                                                                                                                                                             Length 303;
                                                                                                                                                                                                                                                                                            4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 SVYPCRVELDTRSSGRQQWQSIEGTKLSITQGNPSKTQR 159
                                                                                                                                                                                                                                                        Score 821; DB 2;
Pred. No. 1.5e-69;
1; Mismatches 4;
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    19
    note= "signal peptide"

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/note= "mature protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB07443 standard; protein; 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-US030004.
                                                                                                                                                                                                                                                             87.94;
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                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 96.9
Matches 154; Conservative
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N-PSDB; AAA58814.
                                                                                                                                                                                                                               Sequence 303 AA;
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

December 23, 2005, 20:20:08; Search time 12.2093 Seconds (without alignments) 1379.107 Million cell updates/sec Run on:

US-10-780-043-8

Title: Perfect score:

1 MGRPLLLPLLPLLPPAFLQ......KTQRSHWRISGMKDKIQIPS 175 Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR 80:* Database :

piri: * pir2: * pir3: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMEDIPS

	Description	Iq Y heavy chain (겉	Ig heavy chain V r	rearranged T-cell	VpreB protein prec	poliovirus recepto	poliovirus recepto	Ig lambda chain V-	Ig lambda chain -	VpreB protein prec	Ig light chain V r	T-cell receptor de	Ig lambda chain pr	Ig lambda chain pr	Ig lambda chain V-	Ig heavy chain V r	MHC class II I-A-a	T-cell receptor de	m33-B isoform - mo	Ig lambda chain V-	Ig light chain pre	secretory componen	T-cell receptor de	membrane-bound imm	Ig lambda chain V	Ig lambda chain pr	T-cell receptor de	Ig lambda chain pr	eptor tyrosin
SUMMARIES	ΩΙ	i	850065	E27889	146626	A28344	B44194	A44194	S57442	825758	B28344	A55410	836301	PL0114	804937	S16848	D27889	171935	836316	152590	L2HUBH	A31493	QRRBG	836311	A46477	831515	LICHV	836299	S04519	138912
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	Query Match Length	572	1694	118	151	142	392	417	110	235	142	132	131	132	132	136	119	132	142	403	111	125	773	137	226	112	113	145	118	882
de	Query Match	10.9	10.9	10.8	10.8	10.4	10.4	10.4	0	10.3	10.2	10.1	10.0	10.0	10.0	10.0	٠	10.0	10.0	•	6.6	•	٠	9.8	9.8	9.7	9.7	9.7	9.7	9.7
	Score	102	101.5	101	100.5	97	97	97	96.5	96	95.5	94.5	93.5	93.5	93.5	93.5	93	93	93	on.	92.5	92	92	91.5	91.5	91	91	91	90.5	
	Result No.	-	7	М	4	S	v	7	80	0	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

antibody light cha ig lambda chain v- T-cell receptor de ig lambda chain pr T-cell receptor de T-cell receptor de poliovirus recepto poliovirus recepto proteoglycan core ig lambda chain - ig kappa chain - ig heavy chain pre	ig light chain var Ig lambda chain - Ig lambda chain V-
S51149 S44105 S36298 PH0134 S36300 S36317 RWHUPD RWHUPD A28452 S25747 S44122 146638	151216 S14675 L2HUNG
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1110 1110 1112 1140 1140 1108 1108	235 112
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000000000000000000000000000000000000000	88.5 88.5 88.5
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ALIGNMENTS

RESULT

B46529
Ig Y heavy chain (7.88) - duck
N;Alternate names: Ig gamma chain (7.8S)
C;Species: Anas platyrhynchos (domestic duck)
C;Date: 18-Jun-1993 #sequence revision 18-Nov-1994 #text change 21-Jul-2000
C; Accession: B46529; S20759 _
R; Magor, K.E.; Warr, G.W.; Middleton, D.; Wilson, M.R.; Higgins, D.A.
J. Immunol. 149, 2627-2633, 1992
A; Title: Structural relationship between the two IGY of the duck, Anas platyrhynchos: mc
A; Reference number: A46529; MUID: 93017865; PMID: 1401901
A;Accession: B46529
A;Status: preliminary

A; Molecule Lype: mRNA A; Residues: 1-572 <MAG> A; Residues: 1-572 <MAG> A; Cross-rences: UNIPARC:UPI0000116038; EMBL:X65219; NID:g62442; PIDN:CAA46322.1; PIL A; Experimental source: spleen A; Note: sequence extracted from NCBI backbone (NCBIP:116127) C; Superfamily: immunoglobulin C region; immunoglobulin homology C; Keywords: immunoglobulin F;37-120/Domain: immunoglobulin homology <IMM>

Gaps 36; 10.9%; Score 102; DB 2; Length 572; 24.7%; Pred. No. 0.13; tive 29; Mismatches 57; Indels Query Match Best Local Similarity 24.74 Matches 40; Conservative

12 ILLDAAVPGLRAAATLDESGG-----GLVSP-----GGSLTLVCKGSGFTFSSYG 55 5 LLLPLLPLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEI-----PFSFYY 57 ઠે 셤 58 PWELATAPDVRISWRRG--HFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNL 115 ò 셤

116 QKQDQSVYPCRVEL--DIRSSGRQQWQSIEGTKLSITQGNPS 155

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signoachesin - mouse
Gispecies: Mus musculus (house mouse)
Gispecies: Mus musculus (house mouse)
Gispecies: Mus musculus (house mouse)
Gispecies: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
Giscocker. P.R.; Mucklow, S.; Bouckson, V.; McWilliam, A.; Willis, A.C.; Gordon, S.; Mil
EMBO J. 13, 4490-4503, 1994
A;Title: Sialoadhesin, a macrophage sialic acid binding receptor for haemopoietic cells
A;Reference number: S50065, MUID:95009950; PMID:7925291
A;Accession: S50065
A;Status: preliminary
A;Molecule type: mRNA

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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: T-cell receptor
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827889

Ig heavy chain V region (H18-S415) - mouse
C; Species: Mus musculus (house mouse)
C; Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996
C; Accession: 827889
R; Caton, A. J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
EMBO J. S, 1577-1587, 1986
A; Title: Structural and functional implications of a restricted antibody response to a d, Reference number: A91043; MUID:86300658; PMID:2427335
A; Recession: 827889
A; Molecule type: DNA
A; Researce number: A9104000176869
A; Molecule type: DNA
A; Researce UNIPARC:UPI0000176869
A; Reparimental source: strain Balb/c
A; Reparimental source: strain Balb/c
A; Note: this sequence was determined from the germline gene
C; Comment: This chain was isolated from a hybridoma protein that binds influenza virus h
C; Superfamily: immunoglobulin v region; immunoglobulin homology
C; Kaywords: heterotetramer; immunoglobulin
F; 15-97/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rearranged T-cell receptor delta-chain/ Vdeltal.4-Ddeltas-Jdeltal - pig (fragment)
C;8pecies: Sus scrofa domestica (domestic pig)
C;8pecies: 21-Peb-1997 #sequence_revision 21-Feb-1997 #text_change 23-Jul-1999
C;Accession: 146626
R;Yang, Y.G.; Ohta, S.; Yamada, S.; Shimizu, M.; Takagaki, Y.
J. Immunol. 155, 1981-1993, 1995
A;Title: Diversity of T cell receptor delta-chain cDNA in the thymus of a one-month-old A;Reference number: 146623; MUID:95363165; PMID:7636249
A;Accession: 146626
A;Accession: 146626
A;Accession: 146626
A;Reafedus: preliminary; translated from GB/EMBL/DDBJ
A;Reafedus: 1-151 < YAN>
A;Reafedus: 1-151 < YAN>
A;Cross-references: UNIPARC:UPI000011B2A5; GB:D49567; NID:g1041136; PIDN:BAA08511.1; PID
                             PII
A;Residues: 1-1694 <CRO>
A;Cross-references: UNIPROT:Q62230; UNIPARC:UP10000028B74; EMBL:Z36293; NID:g557253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87 PSI----HKDYVNRLFLNWTEGQKSGFLRISNLQKQDQSVYFCRVELDTRSS-----GRQ 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53 DDINYTYYSDSVKGRPTISRDNAKONYTQLSSLKSEDTAMYYC----TRGSYYDYGMD 107
                                                                                                                                                                                                                                                                                  87 PSIHKDYVNRLFLNWTEGOKSGFLRISNLOKODOSVYFCRVELDTRSSGROOMOSIEGTK 146
                                                                                                                                                                                                                                                                                                                . | : | : | : | : | : | | | | 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86
                                                                                                                                                                                                                -----VATIT 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 GVTOPKHLSASMGGSVE-----IPFSFYYPWELATAPDVRISWRRGHFHGQSFYSTRP
                                                                                                                                                                                33 YGVTQPKHLSASMGGSVEIPFSPYYPWELATAPDVRISWRRGHFHGQS-----PYSTRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40;
                                                                                                                                15;
                                                                                Length 1694;
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                                                                                                                                Indels
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                                                                          Match 10.9%; Score 101.5; DB 2; Local Similarity 24.0%; Pred. No. 0.54; es 31; Conservative 26; Mismatches 57;
                                                                             DB 2;
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108 YWG--QGTSVTVS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            138 QWQSIEGTKLSIT 150
                                                                                                                                                                                                                                                                                                                                                                                                                   133 VTVTT-DPS 140
                                                                                                                                                                                                                                                                                                                                                                                        LSITQGNPS 155
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Matches 33; Conserv
                                                                                                                                                                                                                                                                                                                                                                                        147
                                                                          Query Match
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Matches
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A;Cross-references: UNIPROT:P13372; UNIPARC:UP10000003EE4; GB:X05556; GB:X0079; NID:g55 A;Norce: the authors translated the codon GAG for residue 110 as Gln C;Superfamily: immunoglobulin V region; immunoglobulin homology F:20-142/Product: VpreB1 protein #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              poliovirus receptor (clone AGM-delta-1) - green monkey
C;Species: Cercopithecus aethiops (green monkey, grivet)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: B44194
R;Koike, S.; Ise, I.; Sato, Y.; Yonekawa, H.; Gotoh, O.; Nomoto, A.
J. Virol. 66, 7059-7066, 1992
A;Title: A second gene for the African green monkey poliovirus receptor that has no putal
A;Reference number: A44194; MUID:93059651; PMID:1331508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VpreB protein precursor - mouse
CiSpecies: Mus musculus (house mouse)
CiDate: 19-May-1889 #sequence_revision 19-May-1989 #text_change 09-Jul-2004
CiDate: 19-May-1889 #sequence_revision 19-May-1989 #text_change 09-Jul-2004
CiAccession: A2834
Rikudo, A.; Melchers, F.
EMBO J. 6, 2267-2272, 1987
A.Title: A second gene, VpreB in the lambda-5 locus of the mouse, which appears to A.Reference number: A91077; MUID:88029315; PMID:3117530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72 RRGHFHGQSFYST------KPPSIHKDYVNRLFLNWTEGQ-------KS 107
                                                                                                                                                                                                                                                                       DVRISWRRGHFHGQSFYSTRPPSIHKDYV------NRLFLNWTEGQKSGFLRIS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65
                                                                                                                                                                                                                                                                                                         3 LSSLLWLFLTSVF-----SGSGVAQKVTQDQPV-VSRQVGEAVTLNCRYETSWNEYTI- 54
                                                                                                                                     6 LLPLLPLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPPSFYYPWELATAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 LLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWELATAPDVRISW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                       Gaps
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A;Molecule type: DNA
A;Rosidues: 1-392 «KOI>
A;Cross-references: UNIPROT:P32506; UNIPARC:UPI000002B1F7; GB:S48817
C;Superfamily: poliovirus receptor; immunoglobulin homology
F;259-314/Domain: immunoglobulin homology <IMM>
                                                                    35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58;
      Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 142;
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                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ñ
                                                                50;
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Query Match
10.8%; Score 100.5; DB
Best Local Similarity 27.7%; Pred. No. 0.035;
Matches 39; Conservative 17; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                        100 ALQLQDSATYFCALWVVTMSS 120
                                                                                                                                                                                                                                                                                                                                                                                                     114 NLQKQDQSVYFCRVELDTRSS 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Regidues: 1-142 < KUD>
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86 рę

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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: December 23, 2005, 20:19:13 ; Search time 75.5168 Seconds

(without alignments)
1634.967 Million cell updates/sec
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(without alignments)
 1634.967 Million cell updates/
Title: US-10-780-043-8
Perfect score: 934
Sequence: 1 MGRPLLPPLLPPAPLQ......KTQRSHMRISGMKDKIQIPS 175

sequence: 1 MGRPLLLPLLPLLP Scoring table: BLOSUM62

f table: BLOSUM62
Gapop 10.0 , Gapext 0.5
capop 10.0 , Gapext 0.5
sd: 2166443 seqs, 705528306 residues

Searched:

Total number of hits satisfying chosen parameters:

2166443

מי יימווספו כו יוזרם פמרופוליווא כווספכוו

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Listing first 45 summaries
UniProt 05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	рошоч	OHOU	Qsukju nomo sapien Qsbya6 mus musculu	_	Q5w433 brachydanio	homo	рошо	Q69yf9 homo sapien	рошо	tetra	Q62230 mus musculu	O15389 homo sapien	Qépiq7 homo sapien	Q501v7 brachydanio	P13372 mus musculu	Q5w1k4 mus musculu		P32506 cercopithec	Q4t853 tetraodon n	homo	homo	mus m	Q7tmk4 mus musculu	homo	fugr		fugu		Q7yrq7 sus scrofa	Q6pjg0 homo sapien
ID	Q9UKJ1_HUMAN	CENHIL HUMAN	Q8BYA6 MOUSE	Q5W434 BRARE	Q5W433_BRARE	Q8TBC9_HUMAN		Q69YP9_HUMAN	Q9HBS0_HUMAN	Q4T054_TETNG	SN MOUSE	SIGLS HUMAN	Q6PIQ7 HUMAN	Q501V7_BRARE	VPRE1 MOUSE	QSW1K4 MOUSE	Q545E0_MOUSE	PVR_CERAE	Q4T853 TETNG	Q6ZMC9_HUMAN	Q6UXG0_HUMAN		Q7TMK4 MOUSE		QSW431_FUGRU	Q5W436 FUGRU	QSW435_FUGRU	SN HUMAN	Q7YRQ7 PIG	Q6PJG0_HUMAN
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Length	303	977	299	633	651	233	235	149	271	400	1694	551	236	325	142	142	142	417	302	328	394	142	479	360	595	630	648	1709	1730	235
A Query	87.9	9.0	37.2		13.0	11.7	11.1	11.0	11.0	11.0	10.9	10.8	10.7	10.7	10.4	10.4	10.4	10.4	10.3	10.3	10.3	10.2	10.2	10.2	10.2	10.2	10.2	10.2	10.2	10.1
Score	821	143	347	121.5	121.5	109.5	103.5	102.5	102.5	102.5	101.5	100.5	100	100	97	97	97		96	96	96	95.5	٠	95	95	95	95	95	95	94.5
Result No.	н с	N (J 47	ß	9	7	60	o	10	11	12	13	14	15	16	17	. 18	19	20	21	22	23	24	25	56	27	28	53	30	31

RESULT 2 Q8NHI1_HUMAN

O7gaj4 anopheles g	CARMIT MUS MUSCULU	Q6kb05 mus musculu	Q6qi79 rattus norv	Q95kp8 pongo pygma	Q63994 mus musculu	P01706 homo sapien	Q4tbu3 tetraodon n	Q6gnh3 xenopus lae	P01832 oryctolagus	Q8axz4 brachydanio	P11912 homo sapien	P04210 gallus gall	Q6p5s3 homo sapien
010AJ4 ANOGA	CARMIT MOORE	Q6KB05 MOUSE	Q6QI79 RAT	Q95KP8_PONPY	CD33 MOUSE	LV2C HUMAN	Q4TBU3 TETNG	Q6GNH3 XENLA	PIGR RABIT	CNT1A BRARE	CD79A_HUMAN	LV1 CHICK	Q6P5S3_HUMAN
010	V	~	~	~	-	-	~	~	н	7	н	ч	7
358	677	255	1035	269	403	111	172	233	773	1032	226	113	236
1.01	7	10.0	10.0	10.0	10.0	6.6	6.6	6.6	6.6	6.6	8.6	7.6	9.7
94.5		93.5	93.5	93	93	92.5	92.5	92.5	92	92	91.5	91	91

RESELLA RES	SULT 1 OKAJI HUMAN OUNCIL HUMAN OL-MAY-2000 (TERBELEE] 13, Last sequence update) Name-PILRA, Homo saplens (Human) Name-PILRA, Homo saplens (Human) Name-PILRA, Homo saplens (Human) Name-PILRA, Homo saplens (Human) NOCI TAXID-9606; NOCI TAXID-9606
}	
ò	121 SVYPCRVELDTRSSGROQMQSIEGTKLSITQGNPSKTQR 159
q	121 SYYFCRVELDTRSSGRQQWQSIEGTKLSITQAVTTTTQR 159

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61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTBGQKSGFLRISNLQKQDQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                     The German CDNA Consortium;
Pouetka A., Albert R., Mosmayer P., Schupp I., Wellenreuther R.,
Mewes H.W., Well B., Amid C., Osanger A., Pobo G., Han M., Wiemann S.;
Submitted (SEP-2004) to the EMBL/Genbank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MGRPLLLPLILLLQPPAPLQPGGSTGSGPSYLYGVTQPKHLSASMGGSVEIPPSFYYPWE
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STRAIN=C57BL/6J; TISSUE=Thymus;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                      MEDLINE=20127940; PubMed=10660620; DOI=10.1074/jbc.275.6.4467; MOUBBEAU D.D., Barrille D., L'Abbe D., Bouchard P., Shen S.H.; "PILRalpha, a novel immunoreceptor tyrosine-based inhibitory motif-bearing protein, recruite SHP-1 upon tyrosine phosphorylation and is paired with the truncated counterpart PILRbeta.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 SVYPCRVELDTRSSGROOMQSIEGTKLSITQG-----NPSKTQRSHMRISGMK 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus 3 days neonate thymus CDNA, RIKEN full-length enriched
library, clone.A63007P20 product:weakly similar to INHIBITORY
RECEPTOR PILRALPHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Intact, Q9UKJ0; -. Golden to plasma membrane; NAS. GO; GO: 0005887; C: integral to plasma membrane; NAS. GO; 0000518; P: protein binding; IPI. GO; GO: 0007171; P: transmembrane receptor protein tyrosine kin. InterPro; IPR003599; IG. InterPro; IPR007110; IG-11ke.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (SEP-2004) to the EMBL/GenBank/Dubu database.-!- INTERACTION:
095870:BAT5; NDEXP=1; IntAct=EBI-347958, EBI-348517;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PSS0835; IG LIKE; 1.
Hypothetical protein; Immunoglobulin domain; Receptor.
SEQUENCE 227 AA; 25542 MW; 7FF960C60AB7EF09 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79.5%; Score 742.5; DB 81.7%; Pred. No. 3e-62; cive 9; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF161081; AAD52965.1; -; mRNA.
EMBL; AL834336; CAH10711.1; -; mRNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QBBYA6 MOUSE PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 81.7
Matches 143; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                   NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SM00409; IG;
  Name=DKFZp4340079;
                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Testis;
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Nauser R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schafer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schafer C.F., Bhat N.K.,
Altschul R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,
Bitchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Bitchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
Brownstein M.J., Usdin T.B., Tochhyuki S., Carannoi P., Frange C.,
Brownstein M.J., Usdin T.B., Tochhyuki S., Carannoi P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosks S.A., McKwam P.J., McKernan K.J., Makek J.A., Gunzare P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Allalon D.K., Muzny D.M., Sodergren B.J., Lu X., Glibbs R.A.,
Rhiting M., Madan A., Young A.C., Shvychenko Y., Bouffard G.G.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
Butterfield Y.S.N., Warra M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MGRPLLLPLLPLLPPLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE
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01-MAY-2000 (TYEMBLrel. 13, Last sequence update)
01-FEB-2005 (TYEMBLrel. 29, Last annotation update)
Activating receptor PILRbeta (Hypothetical protein DKFZp4340079).
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                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-22388257; PubMed-12477932; DOI-10.1073/pnas.242603899;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.; Strausberg R.; Strausberg R.; Strausberg R.; Submitted (DBC-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC077312; AAH17812.1; -; mRNA. InterPro; IPR003599; IG. InterPro; IPR007110; IG-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00409; IG; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin domain.
SEQUENCE 226 AA; 25479 MW; 5938181797733A30 CRC64;
                                                   Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
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100.0%; Pred. No. 3e-69;
iive 0; Mismatches 0
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                                             01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and mouse cDNA sequences.";
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QSUKJO;
QBNHIL HUMAN PRELIMINARY,
                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                PILRA protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LISSUE-Lung;
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9 9

Gaps

12; Indels

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December 23, 2005, 20:20:23 ; Search time 18.2386 Seconds (without alignments) 793.277 Million cell updates/sec
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1 MGRPLLLPLLPLLPPAFLQ......KTQRSHMRISGMKDKIQIPS 175
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/cgn2_6/ptodata/1/iaa/H_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PGTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
version 5.1.6
- 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                           572060 segs, 82675679 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                     OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                           BLOSUM62
Gapop 10.0 , Gapext 0.5
    GenCore
Copyright (c) 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                      US-10-780-043-8
                                                                                                                                                                                                                                          Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 8, Appli	~	7	7	Sequence 4, Appli		485		754	4,	4	Sequence 79, Appl	77		40	40	57,	40,	16,	16,	16	Seguence 16, Appl	Sequence 5, Appli	8	21.	Sequence 213, App	213,
SUMMARIES	Des			US-09-546-049-2	US-09-869-388-2	JS-09-869-388-4 Se	US-09-869-388-10 Se	85	09-869-388-6	US-09-149-476-754 Se		JS-09-546-049-4 Se	US-08-918-148-79 Se	US-09-138-091A-77 Se			40	7	40	16	9	US-09-364-088-16 Se	9		08-345-321-8 Se			-775A-213
SUMIS	DB ID	1			_	_	2 US-09-8	_	-sn	2 US-09-1	_	_	2 US-08-5	_	_	_	_	2 US-08-8	_	_		2 US-09-3		ns-	us-	_	_	2 US-09-902
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de	Query Score Match	934 100.0				w	'n			517 55		222 23					100 10			٠,			ī.		S	ı,		95 10
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213, A	213, A	213, A	213, A	213, A	213, A		213, A	٠	٠	03	11, Appl	11, Appl	4, App	4, App	4, Appli	7, App	7, Appli	
Sequence	Sequence	Sequence	Sequence	Sequence	Sequence			Sequence				Sequence	Seguence	Sequence	Seguence	Seguence	Seguence	
US-09-906-700-213	US-09-903-603A-213	US-09-904-920A-213	US-09-909-064-213	US-09-905-381A-213	US-09-906-618-213	US-09-906-646-213	US-09-904-462-213	US-09-902-736A-213	US-09-906-722A-213	US-09-949-016-10503	US-08-751-359-11	US-08-907-146-11	US-09-069-821-4	US-09-956-086-4	US-09-956-087-4	US-09-420-592A-7	US-09-985-442-7	ALIGNMENTS
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360	360	360	360	360	360	360	360	360	360	1709	126	126	262	262	262	282	282	
10.2	10.2	10.2	10.2	10.2	10.2	10.2	10.2	10.2	10.2	10.2	10.1	10.1	10.1	10.1	10.1	10.1	10.1	
95	95	95	92	92	92	92	95	92	92	95	94.5	94.5	94.5	94.5	94.5	94.5	94.5	
28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

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Sequence 8, Application US/09869388

Patent No. 6774214

GENERAL INFORMATION:
APPLICANT: Bates, Blizabeth
APPLICANT: Chalus, Lionel
APPLICANT: Garrone, Pierre
APPLICANT: Garrone, Pierre
APPLICANT: CASURION: WONCOTTE-DERIVED NUCLEIC ACIDS AND RELATED COMPOSITIONS AND METHORS.
TITLE REFERENCE: S70977X
CURRENT APPLICATION NUMBER: US/09/869,388
CURRENT PILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: IBM PC compatible
SEQ ID NO 8: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 LATAPDVRISWRRGHPHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQ 120
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Patent No. 6140076
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Adema, Gosse Jan
TITLE OF INVENTION: Isolated Mammalian Monocyte Cell Genes;
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
100.0%; Score 934; DB 2; Length 17
Best Local Similarity 100.0%; Pred. No. 1.4e-89;
Matches 175; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           , ORGANISM: homo sapiens US-09-869-388-8
                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 175
TYPE: PRT
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US-08-985-950-2
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US-09-546-049-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKODO 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MGRPLLLPLLPLLPLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MGRPLLLPLLPLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60
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GENERAL INFORMATION:

APPLICANT: Adema, Gosse Jan
Meyaard, Linde
Gorman, Daniel M.
MCIanahan, Terrill K.
Zurawski, Gerard
Lanier, Lewis L.
Phillips Ur. Joseph H.
TITLE OF INVENTION: Isolated Mammalian Monocyte Cell Genes;
Related Reagents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 303;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 SVYPCRVELDTRSSGROOMQSIEGTKLSITOGNPSKTOR 159
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                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87.9%; Score 821; DB 2; 96.9%; Pred. No. 1.8e-77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSE:
ADDRESSE: JOAX Research Institute
STREET: 901 California Avenue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                  APPLICATION NUMBER: US/08/965,950
FILING DATE: 05-DEC-1997
CLASSIPRICATION: 435
FRIOR APPLICATION: 435
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/041,279
FILING DATE: 21-MARCH-1997
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,181
FILING DATE: 16-DEC-1996
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/032,252
FILING DATE: 06-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAMME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REGISTRATION NUMBER: 34,090
REGISTRATION NUMBER: DX0670K
TELEPHONE: (650)852-9196
                                    ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (650)496-1204
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 303 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 96.9
Matches 154; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-985-950-2
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Sequence 2, Application US/09869388

Sequence 2, Application US/09869388

Patent No. 6774214

GENERAL INFORMATION:
APPLICANT: Bates, Elizabeth
APPLICANT: Chalus, Lionel
APPLICANT: Chalus, Lionel
APPLICANT: Garrone, Pierre
TITLE OF INVENTION: MONOCYTE-DERIVED NUCLEIC ACIDS AND RELATED COMPOSITIONS AND METHO'
TITLE OF INVENTION: WONOCYTE-DERIVED NUCLEIC ACIDS AND RELATED COMPOSITIONS AND METHO'
TITLE OF INVENTION: MONOCYTE-DERIVED NUCLEIC ACIDS AND RELATED COMPOSITIONS AND METHO'
CURRENT APPLICATION UNDER: US/09/869,388
CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: IBM PC compatible
SEQ ID NO 2
IENGTH: 303
TYPE: PRT
CORANISM: homo sapiens
US-09-869-388-2 61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQ 120 61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQ 120 9 1 MGRPLLLPLLPLLPLLPPLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 1 MGRPLLLPLLPLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVBIPFSFYYPWE Gaps ö 87.9%; Score 821; DB 2; Length 303; 96.9%; Pred. No. 1.8e-77; tive 1; Mismatches 4; Indels 121 SVYFCRVELDTRSSGRQQWQSIEGTKLSITQGNPSKTQR 159 121 SVYFCRVELDTRSSGRQQWQSIEGTKLSITQAVTTTTQR 159 PRIOR APPLICATION DAIRS.

PRIOR APPLICATION NUMBER: US/08/985,950
FILING DATE: 05-DEC-1997
APPLICATION NUMBER: US 60/041,279
FILING DATE: 21-MARCH-1997
APPLICATION NUMBER: US 60/033,181
FILING DATE: 16-DEC-1996
ATTORNEY/AGRUT INFORMATION:
REGISTRATION NUMBER: 34,090
REGISTRATION NUMBER: 34,090
REGISTRATION NUMBER: 34,090
REGISTRATION NUMBER: 34,090
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION: TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 2: LENGTH: 303 amino acids TYPE: amino acid TELEFAX: (650)496-1204 INFORMATION FOR SEQ ID NO: 2: Best Local Similarity 96.99 Matches 154; Conservative

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December 23, 2005, 20:40:10 ; Search time 59.5392 Seconds (without alignments) 1228:101 Million cell updates/sec
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934
1 MGRPLILPLLPLLPPAFLQ......KTQRSHMRISGMKDKIQIPS 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Published Applications AA Main:*

(cgn2_6/ptodata/1/pubpāa/USO7_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/USIOA_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/USIOB_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/USIOB_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                  1867569 seqs, 417829326 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                           OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                               Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                   Perfect score:
                                                                                                                                                                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database :
                                                                                                                                                                                                                                                                                             Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                  Searched:
                                                                                                                                            Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		مد			SUMMARIES	
Result No.	Score	Query Match	Query Match Length	DB	αı	Description
1	934	100.0	175	4	US-10-780-043-8	nce 8,
7	821	87.9	303	m	US-09-774-381-58	
e	821	87.9	303	4	US-10-290-631-2	
4	821	87.9	303	4	US-10-780-043-2	7
2	821	87.9	303	4		
9	821	87.9	303	Ŋ	US-10-777-521-2	
7	816	87.4	230	4	US-10-309-290-110	
80	816	87.4	230	4	US-10-780-043-4	
6	809.5	86.7	1012	ហ	US-10-450-763-30868	
10	809.5	86.7	1012	ß	US-10-450-763-33210	
11	809.5	86.7	1012	വ	US-10-450-763-47228	
12	809.5	86.7	1012	ഗ	US-10-450-763-51762	
13	757.5	81.1	226	m	US-09-745-763-106	Sequence 106, App
14	757.5	81.1	226	m	US-09-774-381-44	44,
15	757.5	81.1		4	US-10-780-043-10	10,
16	743.5	79.6		m	US-09-809-391-485	485
17		79.6		m	US-09-882-171-485	485
18	743.5	79.6		4	US-10-164-861-485	485
19	742.5	79.5	227	4	US-10-262-445-128	128,
20	742.5	79.5		4	US-10-780-043-6	ý
21	742.5			Ŋ	US-10-820-474A-7	7,
22	742.5			ش	US-09-935-390A-21	21,
23	742.5			4	US-10-276-774-2380	238
24	655			4	US-10-309-290-112	1
25	517	S	101	m	US-09-809-391-754	754,
56	517	55.4	101	m	US-09-882-171-754	754,
27	517	Ŋ	101	4	US-10-164-861-754	754,

Seguence 711, App	Sequence 4, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 92, Appl	Sequence 184, App	Sequence 158, App	Sequence 168, App	-	Sequence 18, Appl	Sequence 2077, Ap	Sequence 2079, Ap	Sequence 2077, Ap	Sequence 2079, Ap	Sequence 77, Appl	Sequence 48, Appl	Sequence 48, Appl	Sequence 48, Appl
US-09-866-050A-711	US-10-290-631-4	US-10-777-524-4	US-10-777-521-4	US-10-788-625-92	US-10-479-670-184	US-10-479-670-158	US-10-479-670-168	US-10-479-670-174	US-10-779-461-18	US-09-880-748-2077	US-09-880-748-2079	US-10-293-418-2077	US-10-293-418-2079	US-10-778-394-77	US-10-139-785-48	US-10-986-046-48	US-10-986-047-48
m	4	4	'n	ß	4	4	4	4	4	٣	m	4	4	S	4	Ŋ	Ŋ
224	66	66	66	124	253	247	252	253	253	246	246	246	246	244	245	245	245
36.7	23.8	23.8	23.8	12.9	12.5	12.4	12.3	12.3	12.3	11.8	11.8	11.8	11.8	11.7	11.7	11.7	11.7
342.5	222	222	222	120.5	116.5	115.5	114.5	114.5	114.5	110.5	110.5	110.5	110.5	109.5	109.5	109.5	109.5
28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

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APPLICANT: Bates, 1202-043

Sequence 8, Application US/10780043

Publication No. US20040137506A1

GENERAL INFORMATION:
APPLICANT: Bates, Elizabeth
APPLICANT: Chalus, Lional
APPLICANT: Chalus, Lional
APPLICANT: Garrone, Pierre
TITLE OF INVENTION: MONCYTE-DERIVED NUCLEIC ACIDS AND RELATED COMPOSITIONS AND METHE
FILE REFERENCE: SF097X
CURRENT APPLICATION NUMBER: US/10/780,043

CURRENT FILING DATE: 2004-02-17

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 14

SOSTWARE: IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 58, Application US/09774381
Publication No. US20030082677A1
GENERAL INFORMATION:
GENERAL INFORMATION:
Douglas A.
APPLICANT: Holtzman, Douglas A.
APPLICANT: Pan, Yang
APPLICANT: Pan, Yang
APPLICANT: Gearing, David P.
TITLE OF INVENTION: NOVEL EDIRF, MTR-1, LSP-1, TAP-1, AND PA-1 MOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MGRPLLLPLLPLLPPAFLQPSGSTGSGPSYLYGVTQPXHLSASMGGSVEIPFSFYYPWE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 934; DB 4;
100.0%; Pred. No. 5.5e-81;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 175; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 175
TYPE: PRT
ORGANISM: homo sapiens
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US-09-774-381-58
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Gorman, Daniel M.
McClanahan, Terrill K.
Zurawski, Sandra M.
Zurawski, Gerard
Lanler, Lewis L.
Phillips Jr., Joseph H.
Phillips Jr., Joseph H.
Related Mammalian Monocyte Cell Genes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 303
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Pred. No. 6.5e-70;
1; Mismatches 4
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ADDRESSE: DNAX Research Institute
STREF: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
        THILE REPERRICE: MNI-107CP2
CURRENT APPLICATION NUMBER: US/09/774,381
CURRENT PILIDED DATE: 2001-01-30
PRIOR PILING DATE: 1999-09-30
PRIOR PILING DATE: 1999-01-02
PRIOR PILING DATE: 1999-01-02
PRIOR PILING DATE: 1999-01-06
PRIOR PILING DATE: 1999-01-27
PRIOR PILING DATE: 1999-01-27
PRIOR PILING DATE: 1997-10-06
PRIOR PILING DATE: 2000-12-21
PRIOR PILING DATE: 2000-12-21
PRIOR PILING DATE: 1997-10-06
PRIOR PILING DATE: 1997-12-19
PRIOR PILING DATE: 1997-12-19
PRIOR PILING DATE: 2000-01-14
PRIOR PILING DATE: 2000-01-14
PRIOR PILING DATE: 1997-12-19
PRIOR PILING DATE: 2000-01-14
PRIOR PILING DATE: 1997-12-19
PRIOR PILING DATE: 2000-01-14
PRIOR PILING DATE: 1997-12-19
TITLE OF INVENTION: AND USES THEREFOR
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Publication No. US20030105303A1
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APPLICANT: Adema, Gosse Jan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 96.9%;
Matches 154; Conservative
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ORGANISM: Homo sapiens
US-09-774-381-58
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US-10-290-631-2
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Sequence 2, Application US/10780043

Sequence 2, Application No. US20040137506A1

Bublication No. US20040137506A1

GENERAL INFORMATION:
APPLICANT: Bates, Elizabeth
APPLICANT: Chalus, Lionel
APPLICANT: Chalus, Lionel
APPLICANT: Garrone, Pierre
TITLE OF INVENTION: MONCYTE-DERIVED NUCLEIC ACIDS AND RELATED COMPOSITIONS AND METHO
FILE REFERENCE: SF0977X
CURRENT APPLICATION NUMBER: US/10/780,043
CURRENT APPLICATION NUMBER: US/09/869,388
PRIOR FILING DATE: 2002-02-17
PRIOR PILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: IBM PC compatible
SEQ ID NO 2
LENGTH: 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQ 120
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/290,631
FILING DATE: 05-No. US20030105303A1-2002.
CASSIFICATION NUMBER: US/08/985,950
FILING DATE: 05-DEC-1997
APPLICATION NUMBER: US 60/041,279
FILING DATE: 16-DEC-1997
APPLICATION NUMBER: US 60/033,181
FILING DATE: 16-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAMER 16-DEC-1996
ATTORNEY/AGENT INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEFAX: (650)496-1204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-290-631-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Ching, Edwin P. REGISTRATION NUMBER: 34,090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 303 amino acids
TYPE: amino acid
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ORGANISM: homo sapiens
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Sequence 62, Application US/10512184
Publication No. US20050244901A1
GENERAL INFORMATION:
APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.
IITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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Matches
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1819, Ap
1827, Ap
1827, Ap
1927, Ap
1864, Ap
837, App
867, App
867, App
11313, Ap
1787, App
1787,
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64, Appl
63, Appl
65, Appl
2077, Appl
2079, Ap
907, Appl
27, Appl
                                                                                               ); Search time 3.31611 Seconds (without alignments)
376.418 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                934
1 MGRPLLLPLLLPPAFLQ......KTQRSHMRISGMKDKIQIPS 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 26,
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Sequence
Sequence
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'cgn2_6/ptodata/2/pubpaa/USOB NEW PUB.pep:*
'cgn2_6/ptodata/2/pubpaa/USOF NEW PUB.pep:*
'cgn2_6/ptodata/2/pubpaa/PCT_NEW PUB.pep:*
'cgn2_6/ptodata/2/pubpaa/PCT_NEW PUB.pep:*
'cgn2_6/ptodata/2/pubpaa/USIO_NEW PUB.pep:*
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Compugen Ltd
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US-11-054-515-907
US-11-054-515-907
US-11-054-515-1841
US-11-054-515-1827
US-11-054-515-1827
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Sequence 26, Application US/10512184

Sequence 26, Application US/10512184

Publication No. US20050244901A1

GENERAL INFORMATION:
APPLICANT: Praunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.

TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant

TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant

TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant

TITLE OF INVENTION: Antibodies, resistence against fungi

FILE REFERENCE: 3581.01US01

CURRENT FPLILIG DATE: 2004-10-22

NUMBER OF SEQ ID NOS: 72

SEQ ID NO 26

LENGTH: 258
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          76 FHGOSFYSTRPPSIHKDYVNRLFLNWTEGOKSG---FLRISNLOKODOSVYFCRVELDTR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence: scFv CWPD2 OTHER INFORMATION: with specificity against Fusarium ssp.; originates; OTHER INFORMATION: from Gallus gallus.
US-10-512-184-26
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US-11-000-463-346
US-11-054-515-1046
US-11-054-515-1046
US-11-054-515-1053
US-11-054-515-1053
US-11-054-515-1065
US-11-054-515-2065
US-11-054-515-2065
US-11-054-515-942
US-11-054-515-940
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US-10-512-184-64

### Sequence 64, Application US/10512184

### Sequence 64, Application US/10512184

### Sequence 64, Application US/10512184

### Publication No. US20050244901A1

### SENERAL INFORMATION:

### APPLICANT: Fraunhofer Gesellschaft zur P"rderung der angewandten Forschung e.V.

### TITLE OF INVENTION: Antibodies, recombinant

### TITLE OF INVENTION: Antibodies and fusions mediated plant disease

### TITLE OF INVENTION: antibodies and fusions mediated plant disease

### TITLE OF INVENTION: resistance against fungi

### TITLE OF INVENTION: Authority and fusions mediated plant disease

### TITLE OF INVENTION: US01

### TITLE OF INVENTION: Authority and fusions mediated plant disease

### TITLE OF INVENTION: Authority and fusions mediated plant disease

### TITLE OF INVENTION: Authority and fusions mediated plant disease

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CURRENT APPLICATION NUMBER: US/10/512,184
CURRENT FILING DATE: 2004-10-22
NUMBER OF SEQ ID NOS: 72
SEQ ID NO 62
LENGTH: 327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence: precursor OTHER INFORMATION: fusion protein comprising AG - linker - OTHER INFORMATION: scrv CWPD2.
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12.1%; Score 113; DB 6;
Best Local Similarity 31.5%; Pred. No. 0.00064;
Matches 45; Conservative 18; Mismatches 44;
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ORGANISM: Artificial Sequence
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Matches 45; Conserv
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Sequence 63, Application US/10512184

Publication No. US20050244901A1

GENERAL INFORMATION:

APPLICANT: Fraunhofer Gesellschaft zur F*rderung der angewandten Forschung e.V.

APPLICANT: Fraunhofer Gesellschaft zur F*rderung der angewandten Forschung e.V.

TITLE OF INVENTION: antibody fragments and fusions mediated plant disease

TITLE OF INVENTION: antibody fragments and fusions mediated plant disease

TITLE OF INVENTION: resistance against fungi

CURRENT APPLICATION NUMBER: US/10/512,184

CURRENT APPLICATION NUMBER: US/10/512,184

SOFTWARE: PALENTING DATE: 2004-10-22

NUMBER OF SEQ ID NOS: 72

SOFTWARE: PALENTIN Ver. 2.1

SEQ ID NO 633
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Publication No. US20050244901A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
TITLE OF INVENTION: Antibody fragments and fusions mediated plant disease;
TITLE OF INVENTION: Antibody fragments and fusions mediated plant disease;
TITLE OF INVENTION: resistance against fungi
FILE REFERENCE: 3581.010301
CURRENT APPLICATION NUMBER: US/10/512,184
CURRENT FILING DATE: 2004-10-22
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 65
LENGTH: 576
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                                                                                                        December 23, 2005, 20:41:30 ; Search time 4.30146 Seconds (without alignments) 376.418 Million cell updates/sec
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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/cgn2_6/ptodata/2/pubpaa/US10_NEW_FUB.pep:*
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-11-054-515-1131
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Sequence 2.7. Application US/10512184

Sequence 2.7. Application US/20050244901A1

Bublication No. US20050244901A1

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant

TITLE OF INVENTION: antibody fragments and fusions mediated plant disease

TITLE OF INVENTION: antibody fragments and fusions mediated plant disease

TITLE OF INVENTION: antibody fragments and fusions mediated plant disease

TITLE OF INVENTION: antibody fragments and fusions mediated plant disease

TITLE OF INVENTION: antibody fragments and fusions mediated plant disease

TITLE OF INVENTION: antibody fragments and fusions mediated plant disease

TITLE OF INVENTION: antibody fragments and fusions mediated plant disease

TITLE OF INVENTION: antibodies, recombinant antibodies, recombinant disease

TITLE OF INVENTION: antibodies dise
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      1518, Ap
892, App
1957, Ap
1957, Ap
346, App
1719, Ap
1209, Ap
1209, Ap
1250, Ap
1250, Ap
374, App
376, App
376
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Publication No. US2005025532A1
Publication No. US2005025532A1
Publication No. US2005025532A1
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REPERRNCE: PF523P3
CURRENT FAPLICATION NUMBER: US/11/054,515
CURRENT FILING DATE: 2005-02-10
PRIOR APPLICATION NUMBER: 60/543,296
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US-11-054-515-1518
US-10-821-34-892
US-11-054-515-1350
US-11-004-513-1360
US-11-004-513-1360
US-11-054-515-1719
US-11-054-515-1719
US-11-054-515-1250
US-11-054-515-1250
US-11-135-855-36
US-11-135-855-36
US-11-135-855-36
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JS-11-054-515-1328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     128 ELDTRRSGROOLQSIKGTKLTITQAVTTTTWRPSSTTTIA---GLRVTESKGHSESWHL 184
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFREENCE: PF523P3
CURRENT APPLICATION NUMBER: US/11/054,515
CURRENT PILING DATE: 2005-02-10
PRIOR APPLICATION NUMBER: 60/543,296
PRIOR PILING DATE: 2004-02-11
PRIOR PILING DATE: 2004-06-18
PRIOR PILING DATE: 2004-11-14
PRIOR PILING DATE: 2002-11-14
PRIOR PILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR PILING DATE: 2001-11-16
PRIOR PILING DATE: 2001-11-16
PRIOR PILING DATE: 2001-12-19
PRIOR PILING DATE: 2001-06-15
PRIOR PILING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR PILING DATE: 2001-06-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63;
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8.9%; Score 106.5; DB 7; Length 247;
Best Local Similarity 23.7%; Pred. No. 0.0023;
Matches 52; Conservative 26; Mismatches 78; Indels 63
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PRIOR PILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/580,347
PRIOR PILING DATE: 2004-06-18
PRIOR APPLICATION NUMBER: 10/293,418
PRIOR PELING DATE: 2002-11-14
PRIOR PELING DATE: 2001-11-16
PRIOR PELING DATE: 2001-11-16
PRIOR PELING DATE: 2001-12-19
PRIOR PILING DATE: 2001-12-19
PRIOR PILING DATE: 2001-02-19
PRIOR PILING DATE: 2001-02-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR PILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/203,499
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-16
PRIOR PRILING DATE: 2001-03-16
PRIOR PRILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-16
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Publication No. US20050255532A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
US-11-054-515-1294
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PRIOR APPLICATION NUMBER: 62726,248

PRIOR PLING MATERIAN DATE: 60720,816

PRIOR PLING DATE: 60720,817

NUMBER 0 5301 NOS: 327

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OWARY FILMS DURE: 6074146

PRIOR PLING DURE: 60741
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December 23, 2005, 20:40:10 ; Search time 77.2308 Seconds (without alignments) 1228.101 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-780-043-6 1192 Title:

1 MGRPLLLPLLLLLQPPAFLQ......CLLLLWWRRRKGSRAPSSDF 227 Perfect score: Sequence:

1867569 segs, 417829326 residues Gapop 10.0 , Gapext 0.5 Scoring table:

Searched:

BLOSUM62

Total number of hits satisfying chosen parameters:

1867569

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published Applications AA Main:*

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2. /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

3. /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	ΙD	US-10-262-445-128	US-10-780-043-6	US-10-820-474A-7	US-09-935-3904-31	US-10-276-774-2380 X	US-09-774-381-44	US-10-780-043-10	US-09-745-763-106	US-09-809-391-485	US-09-882-171-485	US-10-164-861-485	US-09-774-381-58	US-10-290-631-2	US-10-780-043-2	US-10-777-524-2	US-10-777-521-2	-450-763-	US-10-450-763-33210	US-10-450-763-47228	ç	US-10-309-290-110	US-10-780-043-4	US-10-780-043-8	US-10-309-290-112	US-09-809-391-754	US-09-882-171-754	US-10-164-861-754
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de	Query Match	100.0	100.0	100.0	100.0	100.0	97.6	97.6	97.1	89.7	89.7	89.7	80.4	80.4	80.4	80.4	80.4	63.1	63.1	63.1	63.1	62.4	62.4	62.3	49.7	44.6	44.6	44.6
	Score	1192	1192	1192	1192	1192	1163.5	1163.5	1157.5	1069	1069	1069	958	958	958	958	928	752	752	752	752	744	744	742.5	592	532	532	532
	Result No.	7	7	Μ	,₹	9	Q	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27

Sequence 711, App Sequence 4, Appli Sequence 4, Appli Sequence 6, Appli Sequence 92, Appli Sequence 174, App Sequence 18, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 6, Appli Sequence 18, Appli Sequence 18, Appli Sequence 18, Appli Sequence 18, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli
US-09-866-050A-711 US-110-290-631-4 US-110-777-521-4 US-110-770-521-4 US-110-770-521-4 US-110-770-073-6 US-110-788-625-92 US-110-788-625-92 US-110-788-190-6 US-10-270-073-2 US-10-270-073-2 US-10-270-073-2 US-10-270-11-18 US-10-764-131-2 US-10-764-131-2 US-10-764-131-2 US-10-764-131-2 US-10-764-131-2 US-110-764-131-2 US-110-764-131-2 US-110-764-131-2 US-110-764-131-2 US-110-764-131-2 US-110-77-111
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224 999 999 256 261 261 261 261 252 252 252 310 310
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370 223 223 223 223 120.5 116.5 114 114 1112 1112 1112 1110.5
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APPLICANT GLOC, LOIC
APPLICANT GLOC, Xiaojia
APPLICANT GLOC, Xiaojia
APPLICANT GLOC, Xiaojia
APPLICANT Kevuda, Ramesh
APPLICANT Kevuda, Ramesh
APPLICANT Mises, Peter
APPLICANT Mises, Peter
APPLICANT Mises, Peter
APPLICANT Betuterjain, Weera
APPLICANT Betuter, Rayond J.
APPLICANT BOOG, Chean Bryand J.
APPLICANT BOOG, Maihon
APPLICANT CANDING MISES
APPLICANT BOOG MAINER
APPLICANT CANDING MISES
APPLICANT CON NOWER: 00/227,445
TITLE OF INVENTION: THE SAME
FILE REPERENCE: 2002-10-01
TITLE OF INVENTION WOWER: 00/227,454
FRIOR FILING DATE: 2001-10-05
FRIOR PELICATION NUMBER: 60/328,056
FRIOR PELICATION NUMBER: 60/328,056
FRIOR PELICATION NUMBER: 60/328,056
FRIOR PELICATION NUMBER: 60/328,414
FRIOR PELICATION NUMBER: 60/328,414
FRIOR PELICATION NUMBER: 60/330,142
FRIOR PELICATION NUMBER: 60/330,142
FRIOR PELICATION NUMBER: 60/330,142
FRIOR PELICATION NUMBER: 60/336,289
FRIOR PELICATION NUMBER: 60/336,289
FRIOR PELICATION NUMBER: 60/336,289
FRIOR PELICATION NUMBER: 60/336,369
FRIOR PELICATION NUMBER: 60/336,569
FRIOR PELICATION NU
Sequence 128, Application US/10262445 Publication No. US20040014058A1 GENERAL INFORMATION:
                                                                                                                                  APPLICANT: Alsobrook II, John
APPLICANT: Burgess, Catherine
APPLICANT: Catterton, Blina
APPLICANT: Chant, John
APPLICANT: Chaudhuri, Amtrabha
APPLICANT: Edinger, Shlomit
APPLICANT: Gaciach, Valerie
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APPLICANT:
APPLICANT:
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61 LAIVPNVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQESGFLRISNLRKEDQ 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 SVYPCRVELDTRRSGRQQLQSIKGTKLTITQAVTTTTWRPSSTTTIAGLRVTESKGHSE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MGRPLLLPLLLLLQPPAFLQPGGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: REDDY, ROOPA
APPLICANT: HILLMAN, JENNIFER L.
APPLICANT: HILLMAN, JENNIFER L.
APPLICANT: BANDMAN, OLGA
TITLE OF INVENTION: SIGNAL PEPTIDE-CONTAINING MOLECULES
FILE REFERENCE: 039366-1568
CURRENT APPLICATION NUMBER: 05/720,533
PRIOR PLILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: PCT/US99/14484
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-06-26
PRIOR FILING DATE: 1998-06-26
PRIOR PILING DATE: 1998-06-26
PRIOR PILING DATE: 1998-06-26
PRIOR PILING DATE: 1998-06-26
PRIOR FILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) NAME/KEY: misc feature
) OTHER INFORMATION: Incyte Clone No: 962390
US-10-820-474A-7
                                                                                                         Sequence 7, Application US/10820474A
Publication No. US20050155089A1
GENERAL INFORMATION:
APPLICANT: LAL, PREETI
APPLICANT: CORCONE, GINA A.
APPLICANT: CORLEY, NEIL C.
APPLICANT: GURGOLE, NEIL C.
APPLICANT: GURGOLE, NAIL J.
APPLICANT: BAUGHN, MARIAH R.
APPLICANT: AL-YOUNG, JANICE
APPLICANT: AL-YOUNG, JANICE
APPLICANT: YUE, HENRY
APPLICANT: YUE, HENRY
APPLICANT: PATTERSON, CHANDRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 21, Application US/09935390A; Patent No. US20020076561A1; GENERAL INPORMATION:
APPLICANT: Escobedo, Jaime; Quianjin, Hu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn version 3.3 SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 4
US-09-935-390A-21
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APPLICANT:
APPLICANT:
APPLICANT:
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Squence 6, Application US/10780043
Squence 6, Application US/10780043
Squence 6, Application US/1078043
Squence 6, Application US/107804
GREBEAL INFORMATION:
GREBEAL INFORMATION:
APPLICANT: Browniar, Nathalie
APPLICANT: Chalus, Lionel
APPLICANT: Chalus, Lionel
APPLICANT: Chalus, Lionel
APPLICANT: Granus, Lionel
APPLICANT: Granus, Lionel
APPLICANT: Granus, Lionel
APPLICANT: Granus, Los 103/10/780,043
CURRENT FILING DATE: 2004-02-17
PRIOR APPLICATION NUMBER: US/109/869,388
FRIOR PILING DATE: 2002-02-21
NUMBER PO SEQ ID NOS: 14
SOFTWARE: IBM PC Compatible
SEQ ID NOS: 14
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PRIOR FILING DATE: 2001-10-29
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 133
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 128
LENGTH: 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
                                                                                                                                                                                                                                                                                100.0%; Score 1192; DB 4; Length 227; 100.0%; Pred. No. 6.6e-100; tive 0; Mismatches 0; Indels 0;
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100.0%; Score 1192; DB 4; Length 2
Best Local Similarity 100.0%; Pred. No. 6.6e-100;
Matches 227; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 227; Conservative
                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
US-10-262-445-128
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ORGANISM: homo sapiens
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Novel monocyte-derived polypeptides and polynucleotides, used to diagnose diseases associated with changes in monocyte numbers, e.g. bacterial or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents a human monocyte-derived protein. The specification describes monocyte-derived proteins FDF03, FDF03DeltaTM, FDF03-S1, FDF03-M14, and FDF03-S2. The proteins are involved in the
                                                                                                                                                                                                                                                                                                                                                             Human; monocyte-derived protein; FDF03; FDF03DeltaTM; FDF03-S1;
FDF03-M14; FDF03-S2; haematopoietic cell; monocyte hyperplasia;
tissue rejection; inflammation; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Garrone P;
                                                                                                                                                                                                                                                                                                                                            A human monocyte-derived protein FDF03-S1.
                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .17
/note= "signal sequence"
18. .227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "mature protein"
                  ABG95614
ABG94808
ADH14471
ADH14471
ADH14471
ADH25387
ADH25387
ADH27387
ADH2773
ADH27737
                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 37-38; 45pp; English
                                                                                                                                                                                                                                                                                 AAB07445 standard, protein, 227 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chaulus L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-US030004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-00223919.
                                                                                                                                                                                                                                                                                                                        20-OCT-2000 (first entry)
Bates E, Fournier N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SCHE ) SCHERING CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-465984/40.
N-PSDB; AAA58816.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      viral infections.
           WO200040721-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-DEC-1998;
31-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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362.5
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120.5
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 Abu89624 TNF Tencen Abb12010 Human sec Ady87236 Human sec Ady87236 Human sec Ady87236 Human is Abb07447 A human m Abb53459 Region of Ad12200 Novel hum Ad4202 Human sec Ad474202 Human sec Ad474202 Human sec Ad474202 Human sec Ad521209 Novel hum Abg16869 Novel hum Abg16869 Novel hum Abg16869 Novel hum Abg16869 Novel hum Abg1403 Novel hum Abg1403 Novel hum Abg1403 Novel hum Ad698565 Human imm Ad698565 Human imm Ad698568 Human m Novel Abuman m
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                                                                 20:18:33 ; Search time 94.4367 Seconds (without alignments) 1056.147 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                            1 MGRPLLLPLLLLLQPPAFLQ......CLLLLWWRRRKGSRAPSSDF 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
                                                                                                                                                                                                  2443163
         GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                             2443163 segs, 439378781 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                 - protein search, using sw model
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AABO7447
ABG80407
ABG80407
ABG95345
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ABG95345
ABG95345
ABG772
AABC772
ABG7729
ABG0509
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ABG02851
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Gapop 10.0 , Gapext 0.5
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geneseq2000s:*
geneseq2001s:*
geneseq2001s:*
geneseq2003as:*
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geneseq2003as:*
geneseq2004s:*
                                                                  December 23, 2005,
                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                       US-10-780-043-6
1192
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Match Length DB
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997.7.6
997.1.1
999.7.1
989.7.7
980.7.4
63.11
63.11
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222109974
233109976
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regulation, or development, of haematopoietic cells. Antibodies specific for antigenic components of the proteins can be used to detect the components in samples. The proteins can also be used to screen for candidate therapeutic agents. The monocyte-derived proteins and polynucleotides can be used for diagnosis of diseases related to an increase, or decrease, in the number of monocytes in a tissue or lymph system, such as monocyte hyperplasia, tissue or graft rejection, inflammation, or baccerial or viral infections. The proteins can also be used in the treatment of disorders associated with abnormal expression or
                                                                                                                                                                                                                                                                                                                                                                         LAIVPNVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQESGFLRISNLRKEDQ 120
                                                                                                                                                                                                                                                                                                                                                                                                          LAIVPNVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQESGFLRISNLRKEDQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                            SVYFCRVELDTRRSGRQQLQSIKGTKLTITQAVTTTTTWRPSSTTTIAGLRVTESKGHSE 180
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                                                                                                                                                                                                                                                                                                     MGRPLLLPLLLLLQPPAFLQPGGSTGSGPSYLYGVTQPKHLSASMGGSVBI PFSFYYPWB
                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; cytostatic; DAPK3-Agonist; DAPK3-Antagonist; cancer;
TNF-receptor associated factor 5 interacting protein;
tumour necrosis factor associated factor 5 interacting protein;
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                                                                                                                                                                                                                              Score 1192, DB 3, Length 227; Pred. No. 5e-97; 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TNF-receptor associated factor 5 (TRAF5) interacting protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWHLSLDTAIRVALAVAVLKTVILGILCLILLMWRRRKGSRAPSSDF 227
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09-0CT-2001, 20010S-0328029P.
09-0CT-2001, 20010S-0328056P.
12-0CT-2001, 20010S-0328414P.
15-0CT-2001, 20010S-0329414P.
22-0CT-2001, 20010S-034642P.
24-0CT-2001, 2001US-034629P.
29-0CT-2001, 2001US-034629P.
25-0CT-2001, 2001US-034632P.
25-0CT-2001, 2001US-034632P.
25-0CT-2001, 2001US-034632P.
25-0CT-2002, 2002US-0391342P.
01-0CT-2002, 2002US-0391342P.
                                                                                                                                                                                                                                100.0%;
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2001US-0327917P.
2001US-0328029P.
2001US-0328056P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRAF5 interacting protein.
                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 227, Conservative
                                                                                                                                                              signalling by a monocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CURA-) CURAGEN CORP
                                                                                                                                                                                             Sequence 227 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MGRPLLLPLLLLLQPPAFLQPGGSTGSGPSYLYGVTQPKHLSASMGGSVBIPFSFYYPWE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Secreted protein; human; cell proliferation; cytokine activity; tissue growth; cellular differentiation; regeneration; activin; inhibin; chemotactic; haemostatic; thrombolytic; tumour inhibition; anti-inflammatory activity; blomarker.
                                                                                                                                                                                                        The invention describes an isolated polypeptide comprising any of 33 90-1273 amino acid sequences (I) given in the specification or its mature form, a sequence that is at least 95 % identical to (I), or a sequence comprising one or more conservative substitutions in the amino acid sequence of (I). The polypeptide is useful for preparing a composition for treating or preventing e.g. cancer. This is the amino acid sequence of a tumour necrosis factor (TNP) receptor associated factor 5 (TNP) receptor associated factor 5 (TNP) receptor interacting protein associated with the identification of novel human
                                                                                                                               useful for preparing a composition for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LAIVPNVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTBGQESGFLRISNLRKEDQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Gape
               Kekuda R;
DK, Spytek KA;
 Chaudhuri A;
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                                                                                                                                                                                                                                                                                                                                                                                                         6; Length 227;
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               Guo X,
Rieger
                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 1192; DB 6;
1larity 100.0%; Pred. No. 5e-97;
Conservative 0; Mismatches 0;
Alsobrook JP, Burgess CE, Catterton E, Chan
Edinger SR, Gerlach VL, Glot L, Gorman L,
Racse PS, Millet I, Ooi CE, Patturajan M,
Taupier RJ, Zerhusen BD, Zhong H, Zhong M,
                                                                                                                                                                              Example 20F; Page 242; 253pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW63682 standard; protein; 291
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                                                                                                                                                                                                                                                                                                                                           proteins and their functions
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                                                                                                                                                preventing e.g., cancer.
                                                                                                                               DAPK3 polypeptide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CHIR ) CHIRON CORP
                                                                                WPI; 2003-381704/36
                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
hes 227; Conserv
                                                                                                 N-PSDB; ACA90240
                                                                                                                                                                                                                                                                                                                                                                           Sequence 227 AA;
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Matches
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                       OM protein - protein search, using sw model
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December 23, 2005, 20:20:08; Search time 15.8372 Seconds (without alignments) 1379.107 Million cell updates/sec Run on:

US-10-780-043-6 1192 1 MGRPLLLPLILLLQPPAFLQ.......CLLLLWWRRKKGSRAPSSDF 227

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

283416

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

Database :

PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		propable memorane	m33-B isoform - mo	sialoadhesin - mou	antigen BCM1 precu	ø	poliovirus recepto		PRR2 delta - human	T-cell receptor de	l surface	T-cell surface gly	surface	surface	oda chain	KIAA0992 protein -	CD8 antigen - huma	T-cell surface gly	<u>-</u>	•	m,	e,	ω,	m,	3,		3,	m	-3,	ë,
SUMMARIES		1																													
SUMM	8	100000	240234	152590	850065	JL0143	RWHUPD	RWHUPA	153960	168093	836300	B46482 -	C46482	D46482	T01073	S14675	T13078	139464	825657	A28344	T18390	T18393	T18391	T18394	T18398	T18408	T18405	T18409	T18389	T18392	T18395
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	Query Match		٠,	8.0	8.7	8.6	8.5	8.5	8.4	8.4	8.3	8.3	8.3	8.3	8.3	8.3	8.3	•	8.2	8.1	8.1	8.1	8.1	8.1	8.1	8.1	8.1	8.1	•	8.1	8.1
	Score	130 61	0.027	105.5	104	103	101.5	101.5	100.5	100.5	66	66	66	66	66	98.5	98.5	86	98	76	96.5	96.5	96.5	96.5	96.5	96.5	96.5	96.5	96.5	96.5	96.5
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latrophilin-3, spl poliovirus recepto	T-cell receptor de 1g heavy chain pre VpreB protein prec	Ig heavy chain V r Ig heavy chain V r Ig lambda chain pr	T-cell receptor de Ig heavy chain V-I T-cell surface gly	Ig heavy chain V r T-cell surface gly	hypothetical prote
T18407 B44194 A44194	S36299 B26471 B28344	H30535 D27889 PL0114	S36310 H47624 A30585	PL0252 A34953	876425
000	000	000	0 0 0	000	1 (7)
1580 392 417	145 152 142	122 119 132	142 98 213	213	735
88.1.	88.0 7.9	7.8 8.7 8.8	7.8 7.7 7.7	7.6	7.6
96.5 96 96	95.5 95.5 94	92.5 92.5	92.5 92 91.5	000 000 000 000 000	90.5
30 31	333 343 354	36 37 38	39 41 41	444	45

RESULT 1 S48394 probable membri C;Species: Sac C;Date: 02-Dec C;Accession: S; R;Churcher, C. S;Ubmitted to tl	RESULT 1 S48394 probable membrane protein YIL140w - yeast (Saccharomyces cerevisiae) C;Species: Saccharomyces cerevisiae C;Species: Saccharomyces cerevisiae C;Date: 02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 09-Jul-2004 C;Accession: S48394; S50276 R;Churcher, C. R;Churcher, C. Apumitted to the EMBL Data Library, September 1994 A;Reference number: S48310
A; Access A; Molecu A; Residi A; Cross-	A,Accession: S48394 A,Molecule type: DNA A,Residues: 1-823 <chu> A,Cross-references: UNIPROT:P38928; UNIPARC:UP1000012669C; GB:Z47047; EMBL:Z38059; NID:g</chu>
R; Torpe; Yeast 10 A; Title: A; Refere	R;Torpey, L.E.; Gibbs, P.E.M.; Nelson, J.; Lawrence, C.W. Yeast 10, 1503-1509, 1994 A;Title: Cloning and sequence of REV7, a gene whose function is required for DNA damage-A;Reference number: S50275; MUID:95176709; PMID:7871890
A;Molecule n A;Molecule n A;Residues: A;Cross-refe	A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Mesidues: 80-823 <tor> A;Cross-references: UNIPARC:UP100001689D0; EMBL:U07228; NID:q460247; PIDN:AAA67919.1; Pl</tor>
A,Note: the C,Genetics: A,Gene: SGD A,Cross-ref	A;Note: the nucleotide seguence was submitted to the EMBL Data Library, March 1994 (Senetias: SGD:SRO4 A;Gene: SGD:SRO4 A;Cross-references: SGD:S0001402; MIPS:YIL140w
A, Map pv C, Superi C, Keywol F, 6-22/1	A;Map position: 9L Skuperfamily: Saccharomyces cerevisiae probable membrane protein YIL140w C;Keywords: transmembrane protein F;6-22/Domain: transmembrane #status predicted <tml> F;511-527/Domain: transmembrane #status predicted <tm2></tm2></tml>
Query Best 1 Matche	Query Match Best Local Similarity 23.0%; Pred. No. 0.022; Matches 60; Conservative 43; Mismatches 85; Indels 73; Gaps 15;
ςς O	12 LLQPPAFLQPGGSTGSGPSYLYGV-TQPKHLSASMGGSVEIPFSFYYPWE 60
oy Og	61LAIVPNVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLMWTEGQE 106 ::: :: :: :: :: :: :: :: :: :
ଌ୕ୣ୷ଌ	107 GRFLRISNLRKEDQSVYFCRVELDTR
S G	139 LOSIKGTKLTITQAVTTTTWRPSSTTTIAGLRVTBSKGHSBSWHLSLDTAIRVALAVAV 198

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A; Cross-references: UNIPARC: UP10000176785
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A;Residues: 74-80 <CAB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Accession: S21319
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-240 <WON2>
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950065
stalloadhesin - mouse
C;Specides: Mus musculus (house mouse)
C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: 850065
C;Accession: 850065
A;Title: Sialoadhesin, a macrophage sialic acid binding receptor for haemopoietic cells
A;Reference number: 850065; MUID:95009950; PMID:7925291
A;Reference number: 850065
A;Refere
                                                                                                                                                                                                                                                          m33-B isoform - mouse
CiSpecies: Mus sp. (mouse)
CiSpecies: Mus sp. (mouse)
CiDate: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
CiAccession: 152590
Ritchilan, B.Z.; Beverley, P.C.; Young, B.D.; Watt, S.M.
Blood 83, 3188-3198, 1994
A/Title: Molecular cloning of two isoforms of the murine homolog of the myeloid CD33 ant A/Reference number: 152590, MUID:94250900; PMID:8193354
A/Accession: 152590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ajstatus: preliminary; translated from GB/EMBL/DDBJ
Molecule type: mRNA
AjResidues: 1-403 «FBS»
Ajcross-references: UNIPARC:UPI000020E12; GB:S71345; NID:9551352; PIDN:AAB30842.1; PID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PNVRISWRRGHFHGQS-----FYSTRPPSIHKDYVNRLFLNWTEGQESGFLRISNLRKE 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65 PNVRISW-RRG-HFHGQSFYSTRPPS--IHKDYVNRLFLNWTEGQESGFLRISNLRKEDQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GPVTGSWLRKGVSLHEDSPVATSDPRQLVQKATQGRFQLLGDPQKHDCSLFIRDAQKNDT 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----QA 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    173 TPPTFSWMSTALTSLSSRTTDSSVLTFTPQPQDHGTKLTCLVTFSGAGVTVERTIQLNVT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S LLLPLLLLLQPPAFLQPGGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWELAIV 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----ASVPSLGQTTWGVSSPKNVQGLSGSCLLIPCIFSYPADVPVS 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 LILIPLILLLQPPAFLQPGGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWELAIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 8.9%; Score 105.5; DB 2; Length 403; 1 Similarity 21.8%; Pred. No. 0.18; 63; Conservative 36; Mismatches 103; Indels 87.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1694;
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1 Similarity 22.7%; Pred. No. 1.3;
53; Conservative 32; Mismatches 92; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SVYFCRV--ELDTRRSGRQQLQSIKGTKLTIT-----
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514 PLGVILVALICFLIFWRRRRE 534
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Best Local Similarity
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A.Description: Structure, expression and genetic linkage of the mouse BCM1 (OX45 or Blast 3 region on mouse chromosome 3. A.Reference number: $21319
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A;Title: Identification, by protein sequencing and gene transfection, of sgp-60 as the mm A;Reference number: A47469; MUID:93234508; PMID:8475091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: protein
A; Residues: 84-98 cGA2.
A; Residues: 84-98 cGA2.
A; Residues: 84-98 cGA2.
A; Residues: 84-98 cGA2.
A; Cross-references: UNIPARC: UPI0000176786
A; Cross-references: UNIPARC: UPI0000176786
A; Note: sequence extracted from NCBI backbone (NCBIP:129660)
C; Comment: This antigen is widely expressed on leukocytes and is likely to be anchored to C; Comment: This antigen is widely expressed on leukocytes and is likely to be anchored to C; Superfamily: B-cell surface glycoprotein; lioporotein; phosphatidylinositol linkag F; 1-22/Domain: signal sequence #status predicted <SIG>F; 1-22/Domain: endigen BCMI #status predicted <SIG>F; 1-24/Domain: carboxyl-terminal propeptide #status predicted <CPT>F; 23-237/Pomain: carboxyl-terminal propeptide #status predicted Covalent; #status predicted F; 32, 38, 70, 136, 186, 203/Binding site: carbobydrate (Asn) (covalent) #status predicted F; 217/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Ser) (in mature form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 1-240 <MON>
A;Cross-references: UNIPROT:P18181; UNIPARC:UP10000003EBF; EMBL:X17501; NID:g50134; PIDN
R;Mong, Y.W.; Williams, A.F.; Kingsmore, S.F.; Seldin, M.F.
submitted to the EMBL Data Library, June 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antigen BCM1 precursor - mouse
NiAlternate names: CD48 antigen homolog sgp-60; OX45 antigen, Blast-1 antigen
C;Species: Musculus (house mouse)
C;Species: Musculus (house mouse)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C;Accession: Jiol43; S21319; A47469; B47469
R;Wong, Y.W.; Williams, A.F.; Kingsmore, S.F.; Seldin, M.F.
J. Exp. Med. 171, 2115-2130, 1990
A;Title: Structure, expression, and genetic linkage of the mouse BCM1 (OX45 or Blast-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 PNVRISWRRGHFHGQSF----YSTRPPSIHKDYVNRLFLNWTEGQESGFLRISNLRKEDQ 120
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                                                                                            109 DSGTYNPRPRI----SDSNRWLDVKGT-----TVTVTTDPSPPTITIPEBLR----ECM 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 LLLPLLLLLQPPAFLQPGGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWELAIV 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 LVLELLLL-----PLGTGFQGHSI-----PDINATTGSNVTLKIH-----KDPLG
                                                                                                                                                                                                                                                                                 63; Indels 50;
                                                                                                                                                                                                          179 SESWHLSLDTAIRVALAVAVLKTVILGLLCL----LLLWWRRRKGSRAPSSDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 240;
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A,Note: sequence extracted from NCBI backbone (NCBIP:129658)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            region on mouse chromosome 3.
A;Reference number: JL0143; MUID:90278362; PMID:1693656
A;Accession: JL0143
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Best Local Similarity 23.6%; Pred. No. 0.16;
Matches 45; Conservative 33; Mismatches
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December 23, 2005, 20:19:13; Search time 97.9561 Seconds (without alignments) 1634.967 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                        OM protein - protein search, using sw model
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US-10-780-043-6 1192 1 MGRPLLLPLLLLLQPPAFLQ.......CLLLLWWRRKKGSRAPSSDF 227 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2166443 seqs, 705528306 residues Searched:

2166443 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	Q9ukj0 homo sapien	homo	homo	Q8bya6 mus musculu	Q5w434 brachydanio	Q5w433 brachydanio	P38928 saccharomyc	Q69yf9 homo sapien		Q755vl ashbya goss		Q9by67 homo sapien	mus	Q8r411 mus musculu	mus	Q62230 mus musculu	Q8tbc9 homo sapien	Q7yuq4 trypanosoma	mus	P18181 mus musculu	Q545k2 mus musculu	-	-		_		Q5dwn6 eptatretus	Q7yuq1 trypanosoma	Q5r1x6 rattus norv		Q4kcc5 pseudomonas
SUMMARIES		QΙ	Q9UKJO HUMAN	Q9UKJ1_HUMAN	Q8NHI1 HUMAN	Q8BYA6 MOUSE	QSW434_BRARE	Q5W433_BRARE	AXL2 YEAST	Q69YF9 HUMAN	Q9HBS0_HUMAN	Q755V1_ASHGO	Q4IJC5 GIBZE	Q9BY67 HUMAN	Q9Z2H8_MOUSE	Q8R4L1_MOUSE	CD33_MOUSE	SN MOUSE	Q8TBC9 HUMAN	Q7YUQ4_9TRYP	Q8K3T6_MOUSE	CD48_MOUSE	Q545K2_MOUSE	Q6P905_MOUSE	GATAS_HUMAN	Q86VU4_HUMAN	Q8C2T1_MOUSE	QSDWNS EPTBU	QSDWN6_EPTBU	Q7YUQ1 9TRYP	QSR1X6_RAT	Q7YUQ2_9TRYP	Q4KCC5_PSEF5
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		Match Length	227	303	226	299	633	651	823	149	271	831	275	442	295	445	403	1694	233	369	445	240	240	240	397	417	151	283	283	369	359	369	370
	Query	Match	100.0	80.4	62.4	34.4	10.4	10.4	10.1	9.9	9.6	9.7	9.3	9.0	6.8	8.9	9.9	8.7	8.7	8.7	8.7	9.6	8.6	8.6	8.6	8.6	9.8	9.8	9.8	9.8	8.5	8.5	8.5
		Score	1192	928	744	410	123.5	123.5	120.5	118	118	115.5	111	107.5	106.5	106.5	105.5	104	103.5	103.5	103.5	103	103	103	103	103	102.5	102.5	102.5	102.5	101.5	101.5	101.5
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P15151 homo sapien Q5w431 fugu rubrip Q5w436 fugu rubrip	Q5w43s fugu rubrip Q6piq7 homo sapien Q60hi1 eptatretus Q7yuq3 trypanosoma		Q6qx36 mus musculu Q8ax17 oncorhynchu Q80wm5 mus musculu
PVR HUMAN QSW431 FUGRU QSW436 FUGRU	Q5W435_FUGRU Q6PIQ7_HUMAN Q60HI1_EPTBU Q7YUQ3_9TRYP	Volees Human PVR2 Human Q819K3 BRAFL Q08835_CERAE	Q6QX36_MOUSE Q8AXL7_ONCMY HPLN3_MOUSE
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                                                                                                  61 LAIVPNVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQESGFLRISNLRKEDQ 120
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LAIVPNVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQESGFLRISNLRKEDQ 120
                                                              SVYFCRVELDTRRSGRQQLQSIKGTKLTITQAVTTTTTWRPSSTTTIAGLRVTESKGHSE 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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80.8%; Pred. No. 1.8e-79;
ive 15; Mismatches 19; Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            173 TESKGHSESWHLSLDTAIRVALAVAVLKTVILGLLCLLLLWWRRRKGSR 221
                                                                                                                                                                                           SWHLSLDTAIRVALAVAVLKTVILGLLCLLLLWWRRRKGSRAPSSDF 227
                                                                                                                                                                                                                            SWHLSLDTAIRVALAVAVLKTVILGLLCLLLLWWRRRKGSRAPSSDF 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunoglobulin domain; Receptor.
SEQUENCE 303 AA; 33878 MW; 0410ADFC7E80928B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAX-2004 (TrEMBLrel. 26, Last annotation update)
Inhibitory receptor FILRalpha.
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QBNHII;
01-OCT-2002 (TrEMBLrel. 22
01-OCT-2002 (TrEMBLrel. 22
                                                                                                                                                                                                                                                                                                                                                                                                           QQUKJ1 HUMAN PRELIMINARY,
QQUKJ1,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=PILRA;
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RX MELLURG;

RA MEDILINE_2298257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA MELLURE_2298257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Alschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Alschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Alschul S.F., Jordan H., Moore T., Mang J., Hsieh F.,

RA Alschul S.F., Jordan H., Moore T., Marx S.I., Wang J., Hsieh F.,

RA Alschul S.F., Jordan H., Moore T., Marx S.I., Wang J., Hsieh F.,

RA Alschul S.F., Jordan H., Ponaldo M.F., Casavant T.L., Scheetz T.E.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Carainci P., Frange C.,

RA Raha S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Riching M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

Ra Generation and initial analysis of more than 15,000 full-length human
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                                                                        Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MGRPLLLPLLLLLQPPAFLQPGGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE
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01-MMR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A630007P20 product:weakly similar to INHIBITORY RRCEPTOR PILAALPHA.
Name-POLTA, Synonyms-AV021745;
Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.; Submitted (DRC-2001) to the EMBL/GenBank/DDBJ databases. Submitted (DRC-2001) to the EMBL; BC017812; AAH17812.1; -; mRNA. INTEFPC; IPR003599; IG. InterPro; IPR007599; IG. InterPro; IPR007110; IG-like. SMART; SM00409; IG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 SVYFCRVELDTRRSGROOLQSIKGTKLTITQAVTTTTWRPS 162
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SEQUENCE 226 AA; 25479 MW; 5938181797733A30 CRC64;
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Sequence 8, Appli
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Sequence 6729, Ap Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 6278, Ap Sequence 66, Appl Sequence 66, Appl Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl Sequence 5, Appl Sequence 5, Appl Sequence 5, Appl Sequence 10, Appl		Seguence 6, Application US/09869388 Sequence 6, Application US/09869388 Sequence 6, Application US/09869388 Setent No. 6774214 SENERAL INFORMATION: APPLICANT: Bates, Elizabeth APPLICANT: Fournier, Nathalie APPLICANT: Chalus, Lional APPLICANT: Chalus, Lional APPLICANT: Garrone, Pierre APPLICANT: Garrone, Pierre APPLICANT: ON MONGYTE-DERIVED NUCLEIC ACIDS AND RELATED COMPOSITIONS AND METH FILE REFERENCE: SF09 MONGYTE-DERIVED NUMBER: US/09/869,388 CURRENT APPLICATION NUMBER: US/09/869,388 CURRENT FILING DATE: 2002-02-21 SOFTWARE: IBM PC compatible SEQ ID NO 6 SEQ ID NO 6 SEQ ID NO 6 SECTION NUMBER: US/09/869,388 SOFTWARE: LENGTH NUMBER: US/09/869,388 SOFTWARE: LENGTH NUMBER: US/09/869,388 SOFTWARE: LENGTH NUMBER: US/09/869,388	3 2; Length 227; 114; Indels 0; Gaps 0;	MGRPLLLPLLLLQPPAFLQPGGSTGSGPSYLXGVTQPKHLSASMGGSVBIPFSFYYPWE 60 	LAIVPNVRISWRRGHFHGGSFYSTRPPSIHKDYVNRLFLNWTEGGESGFLRISNLRKEDQ 120 	SVYFCRVELDTRRSGRQQLQSIKGTKLTITQAVTTTTWRPSSTTTIAGLRVTESKGHSB 180 	RKGSBAPSSDF 227 RKGSBAPSSDF 227	
US-09-949-016-6729 US-09-260-527-1 US-09-249-016-7564 US-09-249-016-7567 US-09-949-016-7567 US-09-949-016-7567 US-09-949-016-7567 US-09-453-234-66 US-09-453-234-66 US-09-453-234-66 US-08-453-234-66 US-08-453-234-66 US-08-453-234-70 US-08-453-234-70 US-08-559-628-2 US-08-559-628-2 US-08-559-628-2 US-08-559-628-2 US-08-559-628-2 US-08-53-234-70 US-09-456-0108-7	ALIGNMENTS	69388 e DERIVED NUCLEIC AC S/09/869,388 -21	; Score 1192; DB 2; ; Pred. No. 1.5e-114; 0; Mismatches 0;	LQPGGSTGSGPSYLYGVT LQPGGSTGSGPSYLYGVT	OSFYSTRPPSIHKDYVNR 	LOSIKGTKLTITOAVTTT LOSIKGTKLTITOAVTTT	SWHLSLDTAIRVALAVAVLKTVILGLLCLLLLWWRRRKGSRAPSSDF 	869388 e
8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8		SULT 1 -09-869-388-6 Sequence 6, Application US/09869388 Patent No. 6774214 APPLICANT: Bates Elizabeth APPLICANT: Fournier, Nathalie APPLICANT: Fournier, Nathalie APPLICANT: Garrone, Pierre TILLE OF INVENTION: MONOCYTE-DERIV TILLE OF INVENTION: MONOCYTE-DERIV CURRENT PILING DATE: 2002-02-11 SUMMER OF SEQ ID NOS: 14 SOFTWARE: IBM PC Compatible SEQ ID NO 6 LENGTH: 227 TYPE: PRT ORGANISM: homo sapiens	100.0%; ilarity 100.0%; Conservative	RPLLLPLLLLLQPPAF) RPLLLPLLLLQPPAF)	IVPNVRISWRRGHFHG(YFCRVELDTRRSGRQQ) YFCRVELDTRRSGRQQ)	HLSLDTAIRVALAVAVI HLSLDTAIRVALAVAVI	tion US/09 lizabeth r, Nathali Lionel
1011.5 1011.5 1000.5 10		SULT 1 Sequence 6, Application Parent No. 674214 GENERAL INFORMATION: APPLICANT: Bates, Eliza APPLICANT: Bates, Eliza APPLICANT: Chalus, Lio APPLICANT: Chalus, Lio APPLICANT: Garrone, Pi TITLE REFERENCE: POUTIEN, LIO CURRENT APPLICATION NUM CURRENT APPLICATION NUM CURRENT PILING DATE: 2 NUMBER OF SEQ ID NOS: 1 SOFTWARE: IBM PC compat LENGTH: 227 TYPE: PRT TYPE: PR	Query Match Best Local Similarity Matches 227; Conser	1 MG	61 LA 61 LA	121 SV 	181 SW 	RESULT 2 'US-09-869-388-10 'Sequence 10, Applica 'Patent No. 6774214 'GENERAL INFORMATION: 'APPLICANT: Bates, B 'APPLICANT: Fournie 'APPLICANT: Chalus,
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R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,592
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R APPLICATION NUMBER: 60/047,584
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APPLICATION NUMBER: 60/043,312
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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,872
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APPLICATION NUMBER: 60/047,500
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APPLICATION NUMBER: 60/047,492
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APPLICATION NUMBER: 60/047,582
FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/043,314
FILING DATE: 1997-04-11
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APPLICATION NUMBER: 60/043,674
FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,669
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FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,315
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FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/056,886
FILING DATE: 1997-08-22
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APPLICATION NUMBER: 60/056,893
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                                                                                                                                                                                                           60/047,618
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APPLICATION NUMBER: 60/047,503
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APPLICATION NUMBER: 60/047,613
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APPLICATION NUMBER: 60/047,601
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APPLICATION NUMBER: 60/043,311
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UB-10-78

TITLE OF INVENTION: MONOCYTE-DERIVED NUCLEIC ACIDS AND RELATED COMPOSITIONS AND METHO
FILE REPERENCE: SP0977X
GURRENT APPLICATION NUMBER: US/09/869,388
CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 14
SQOTWARE: IBM PC compatible
SQOTWARE: 10N 0.10
LENGTH: 226
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Pred. No. 1.3e-111;
1; Mismatches 2; Indels
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Patent No. 6420526
GENERAL INPORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 186
FILE REFERENCE: PZ002P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT PEPLICATION NUMBER: US/09/149,476
CURRENT PELING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: US/09/149,476
CURRENT FILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER PELING DATE: 1997-05-23
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FILING DATE: 1997-05-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 98.2%;
Matches 223; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -09-149-476-485
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AAX87230 AAW75053 AAW75053 ABW75053 ABW73469 ABW723469 AAW5237 AAW19872 ABW97118 ABW97118 ABW71520 ABW71520

Human pro
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ALIGNMENTS

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AAB07444 standard; protein; 230 AA
RESULT 1
AAB07444
ID AAB0
Aab67444 A human m
Ade55578 Human NOV
Ade55129 PRO polyp
Ade5580 Human m
Ad555129 PRO polyp
Ad69558 Human nov
Ad695580 Human nov
Abg02851 Novel hum
Abg02851 Novel hum
Abg02851 Novel hum
Abg02851 Novel hum
Abg01403 Novel hum
Aaw8040746 A human m
Aaw80407 A secrete
Abg6185 Human ESP
Ad96815 Human isP
Ad96815 Human isP
Ad96915 Human isP
Ad96915 Human isP
Ad969145 A human m
Abg95345 Human isP
Ad12200 Novel hum
Abd95345 Human isP
Ad12200 Novel hum
Abd98924 TNF-recep
Ad52200 Human sec
Adb7445 A human m
Abu88924 TNF-recep
                                                                  December 23, 2005, 20:18:33 ; Search time 95.6848 Seconds (without alignments) 1056.147 Million cell updates/sec
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                                                                                                           US-10-780-043-4
1223
1 MGRPLLLPLLPLLPPAPLQ......PSHRPLKSPQNETLYSVLKA 230
         5.1.6
Compugen Ltd
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                                                                                                                                                                                     2443163 segs, 439378781 residues
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         GenCore version (c) 1993 - 2005
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Maximum Match 100%
Listing first 45 summaries
                                                protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB
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\$ \$ \$	AAB07444;	
\$ E \$	20-OCT-2000 ((first entry)
智	A human monocy	A human monocyte-derived protein FDF03DeltaTM.
333 3	Human; monocyt FDF03-M14; FDF tissue rejecti	Human, monocyte-derived protein, FDF03; FDF03DeltaTM, FDF03-S1; FDF03-M14; FDF03-S2; haematopoietic cell; monocyte hyperplasia; tissue rejection; inflammation; infection.
38 3	Homo sapiens.	
iet i	Key Peptide	Location/Qualifiers 1. 17 /note= "eimal mantide"
H	Protein	/note= "mature protein"
X & I	WO200040721-A1	
X & !	13-JUL-2000.	
ž & !	29-DEC-1999;	99WO-US030004.
X	31-DEC-1998; 31-DEC-1998;	98US-00223919. 98US-00224604.
:	(SCHE) SCHERI	SCHERING CORP.
E E	Bates E, Four	Fournier N, Chaulus L, Garrone P;
388 3	WPI; 2000-465984/40. N-PSDB; AAA58815.	84/40. 15.
{	Novel monocyte-de diseases associat viral infections.	Novel monocyte-derived polypeptides and polynucleotides, used to diagnose diseases associated with changes in monocyte numbers, e.g. bacterial or viral infections.
\$ E \$	Claim 1; Page	Claim 1; Page 34-35; 45pp; English.
\$888	The present se specification FDF03-S1, FDF0	The present sequence represents a human monocyte-derived protein. The specification describes monocyte-derived proteins FDF03, FDF03DeltaTM, FDF03-S1, FDF03-M14, and FDF03-S2. The proteins are involved in the

AMB07443 ADP25129 ADP25129 ADF25129 ADF20509 ABG060509 ABG02851 ABG02851 ABG02851 AABG1446 AAW080407 AAY08015 AAY08 AAY0

303 303 303 303 303 303 1012 1012 1012 228 228 228 228 223 223 326 327 327 327

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ragulation, or development, of haematopoietic cells. Antibodies specific for antigenic components of the proteins can be used to detect the components in samples. The proteins can also be used to screen for candidate therapeutic agents. The monocyte-derived proteins and polymucleotides can be used for diagnosis of diseases related to an increase, or decrease, in the number of monocytes in a tissue or lymph system, such as monocyte hyperplasia, tissue or graft rejection, inflammation, or bacterial or viral infections. The proteins can also be signalling by a monocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 SVYFCRVELDTRSSGROOWGSIEGTKLSITOGOORTKATTPAREPFONTEEPYENIRNEG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SVYFCRVELDTRSSGROOMQSIEGTKLSITQGQQRTKATTPAREPFQNTEEPYENIRNEG 180
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                                                                                                                                                                                                                                                                                                                         1 MGRPLLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE
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2001US-0341540P.
2001US-0342592P.
2001US-0344297P.
2001US-0344903P.
2002US-0373288P.
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2001US-0341346P.
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                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0
Matches 230; Conservative
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                                                                                                                                                                                                               Sequence 230 AA;
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17-APR-2002;
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12-DEC-2001;
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This invention relates to novel NOVX proteins, and the DNA sequence which encode them, having properties related to stimulation of biochemical or physiological responses in a cell, a tissue, an organ or an organism.

Compounds which modulate the proteins of the invention may have cardiant. Compounds which modulate the proteins of the invention may have cardiant. In the modulate in expression of the invention may have cardiant. Immunosuppressive, anti-HIV, antinflammatory, neuroprotective, neuroleptic, antidepressant, antidathmanian, antidathmatic, neuroleptic, antidepressant, antidathmanian, antidathmatic, neuroleptic, antidepressant, antidathmany be useful for gene therapy whilst the protein sequences of the invention may be useful for gene therapy whilst the protein sequences of the invention may be useful for gene therapy whilst the protein sequences of the invention may be useful for gene therapy whilst the protein sequence of the invention may be useful for gene therapy whilst the protein is useful in the manufacture of a medicament for treating a syndrome associated with a human disease. The invention may be useful in the manufacture of a medicament for cardiomyopathy, atherosclerosis, hypertension, cancer, obesity, cheumatod, atthritis, adiabetes, glomerulonephritis, postiasis, skin disease, asthma, schizophrenia, depression, allergies or cardiomyopathy and probes, in chromosome mapping, tissue typing, preventive medicine, and pharmacogenomics. The present sequence is the amino acid sequence of the human NOVXIBa protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New NOVX polypeptides and nucleic acids, useful for preventing or treating NOVX-associated disorders, e.g. cancer, cardiomyopathy, atherosclerosis or diabetes, and in chromosome mapping, tissue typing or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MGRPLLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 2; SEQ ID NO 110; 211pp; English.
                 17-MAY-2002; 2002US-0381495P.
28-MAY-2002; 2002US-0383534P.
28-MAY-2002; 2002US-0383534P.
29-MAY-2002; 2002US-038329P.
29-MAY-2002; 2002US-0384024P.
07-AUG-2002; 2002US-0401788P.
26-AUG-2002; 2002US-0406353P.
02-DEC-2002; 2002US-0406353P.
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Matches 229; Conservative
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

December 23, 2005, 20:20:08; Search time 16.0465 Seconds (without alignments) 1379:107 Million cell updates/sec Run on:

US-10-780-043-4 1223 Perfect acore:

1 MGRPLLLPLLPLLPPAFLQ......PSHRPLKSPQNETLYSVLKA 230 Sequence:

BLOSUM62 Scoring table:

283416 seqs, 96216763 residues Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters:

283416

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 80:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:* 4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	sialoadhesin - mou	Iq Y heavy chain (Ig heavy chain V r		Ig lambda chain -	receptor tyrosine	colon carcinoma-as	probable neural ce	Ig gamma-2 chain -	VpreB protein prec	Ig lambda chain V-	elastic titin - hu	membrane-bound imm	VpreB protein prec	Ig heavy chain pre	Ig light chain V r	protein-tyrosine k	T-cell receptor de	Ig lambda chain pr	g lambda chain	heavy chain N	MHC class II I-A-a	rearranged T-cell	T-cell receptor de	antigen BCM1 precu		-	Ig lambda chain V-	Ig lambda chain V-
SUMMARIES	ID	\$50065	B46529	E27889	146626	S25758	138912	A54017	T42718	833598	A28344	S57442	I38346	A46477	B28344	B26471	A55410	A53743	S36301	PL0114	S04937	D27889	171935	146638	836316	JL0143	152590	I38344	L2HUBH	S16848
	Length DB	694 2	572 2	118 2	•	235 2	•	416 2	•	135 2	•	•	7962 2	•	142 2	152 2	132 2	890 1	••	32	32	•	•	140 2	•	•	403 2	6926 1	111 1	136 2
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de	Query Match		æ	æο						-	,		-	•		•			7		-	7	7	7	_	7	7	7.	7.	7
	Score	109	104.5	101	100.5	66	98	97.5	97.5	97	97	96.5	96.5	96	95.5	95.5	94.5	94	93.5	93.5	93.5	93	93	93	93	93	93	93	92.5	92.5
	Result No.	-	71	М	4	ហ	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

Ig light chain pre	T-cell receptor de	Ig lambda chain -	Ig lambda chain V	Ig lambda chain pr	T-cell receptor de	Ig lambda chain pr	Ig lambda chain -	antibody light cha	Ig lambda chain V-	T-cell receptor de	T-cell receptor de	T-cell receptor de	protein-tyrosine k	receptor tyrosine	proteoglycan core
A31493	836311	S25747	831515	LICHV	836299	804519	S14675	851149	S44105	836298	836300	836317	JC4166	178875	A28452
7	~	0	0	н	N	~	~	~	7	~	~	~	-1	~	0
125	137	233	112	113	145	118	235	110	112	135	143	149	880	1333	2124
7.5	7.5	7.5	7.4	7.4	7.4	7.4	7.4	7.4	7.4	7.4	7.4	7.4	7.4	7.4	7.4
92	91.5	91.5	91	91	91	90.5	90.5	06	90	06	06	90	90	90	90
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	5

ALIGNMENTS

RESULT 1
S50065
sialoadhesin - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-May-1995 #sequence revision 21-Jul-1995 #text change 09-Jul-2004
C;Accession: S50065
R;Crocker, P.R.; Mucklow, S.; Bouckson, V.; McWilliam, A.; Willis, A.C.; Gordon, S.; Mil
EMBO J. 13, 4490-4503, 1994
Arritle: Sialoadhesin, a macrophage sialic acid binding receptor for haemopoietic cells
A; Reference number: S50065; MUID:95009950; PMID:7925291
A; Accession: S50065
A;Status: preliminary

A; Molecule type: mRNA

A;Residues: 1-1694 <CRO> A;Cross-references: UNIPROT:Q62230; UNIPARC:UPI0000028B74; EMBL:Z36293; NID:g557253; PII

ë Gaps 24; Query Match
8.9%; Score 109; DB 2; Length 1694;
Best Local Similarity 22.5%; Pred. No. 0.86;
Matches 38; Conservative 30; Mismatches 77; Indels 2.

98 33 YGVTQPKHLSASMGGSVEIPPSFYYPWELATAPDVRISWRRGHFHGQS-----PYSTRP ð

87 PSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQSVYFCRVELDTRSSGRQQWQSIEGTK 146 16 셤 ઠે

147 LSITQGQQRTKATTP--AREPFQ---NTEEPY----ENIRNEGQNTDP 185 g ò

181 133 VIVITDPSPPTITIPEELREGMERNFNCSTPYLCLQEKQVSLQWRGQDP

g

Ig Y heavy chain (7.8S) - duck

NyAlternate names: I gamma chain (7.88)
C;Species: Anas platyrhynchos (domestic duck)
C;Species: Anas platyrhynchos (domestic duck)
C;Date: 18-Unn-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C;Accession: B46529; S20759
R,Magor, K.B.; Marr, G.W.; Middleton, D.; Wilson, M.R.; Higgins, D.A.
J. Immunol. 149, 2627-2633, 1992
A;Title: Structural relationship between the two IgY of the duck, Anas platyrhynchos: mcA;Reference number: A46529; MUID:93017865; PMID:1401901

A;Status: preliminary
A;Rolecule type: mRNA
A;Rolecule type: mRNA
A;Residues: 1-572 <MAGA
A;Cross-references: UNIPARC:UP10000116038; EMBL:X65219; NID:g62442; PIDN:CAA46322.1; PII
A;Experimental source: spleen
A;Note: sequence extracted from NCBI backbone (NCBIP:116127)
C;Superfamily: immunoglobulin C region; immunoglobulin homology

N

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A;Molecule type: mRNA
A;Residues: 1-151 <YAN>
A;Residues: 1-151 <YAN>
A;Cross-recences: UNIPARC:UPI000011B2A5; GB:D49567; NID:g10411136; PIDN:BAA08511.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CjAccession: S25758
K. Combriato, G.; Klobeck, H.G.
Bur. J. Immunol. 21, 1513-1522, 1991
A;Title: Vilambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam: A;Reference number: S16439; MUID:91257162; PMID:1904362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPARC:UPI0000115F06; EMBL:X57823; NID:g33745; PIDN:CAA40960.1; PID CS.Superfamily: immunoglobulin vegion; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin homology <IMMN-F:150-218/Domain: immunoglobulin homology <IMMN-F:150-218/Do
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cipate: 29-May-1998 #sequence_revision 29-May-1998 #text_change 05-Oct-2004
Cipate: 29-May-1998 #sequence_revision 29-May-1998 #text_change 05-Oct-2004
Cipate: 29-May-1998 #sequence_revision 29-May-1998 #text_change 05-Oct-2004
Ricrosier, K.B.; Hall, L.R.; Lewis, P.M.; Morris, C.M.; Wood, C.R.; Morris, J.C.; Crosie Ricrosier, K.B.; Hall, L.R.; Lewis, P.M.; Morris, C.M.; Wood, C.R.; Morris, J.C.; Crosie Rythite: Isolation and characterization of the human DTK receptor tyrosine kinase.
A;Reference number: I38912
A;Accession: I38912
A;Accession: I38912
A;Accession: I38912
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86 PPSIHK----DYVNRL--FLNWTEGQKSG---FLRISNLQKQDQSVYFCRVELDTRSSGR 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PGKAPKIMIYDVTNRPSGVSNRFSGSKSGNTASLTISGLQPEDEADYYC----TSKTSS 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 DVRISWRRGHFHGQSFYSTRPPSIHKDYV------NRLPLNWTEGQKSGFLRIS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 LLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWELATAP 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig lambda chain - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 GIGSWAQSALTQPASVSGSPGQSITISCT-----GSSSDV-----GGYNYVSWYQQH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26 GSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWELATAPDVRISWRRGHFHGQSFYSTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32,
                                                                                                                                                                                                                                                                     Length 151;
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                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                     8.2%; Score 100.5; DB 2; 27.7%; Pred. No. 0.2;
                                                                                                                                                                                                                                                                                                                                              20,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    137 QOWQSIEGTKLSITQGQQRTKATT----PAREPFQ 167
    A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                      17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20, Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100 ALQLQDSATYFCALWVVTMSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                114 NLQKQDQSVYFCRVELDTRSS 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 28.4%;
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                                                                                                                                                                                                                                                                                                             Local Similarity 27.7% hes 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1-235 <COM>
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14626
rearranged T-cell receptor delta-chain/ Vdeltal.4-Ddeltas-Jdeltal - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 23-Jul-1999
C;Accession: 14626
R;Yang, Y.G.; Ohta, S.; Yamada, S.; Shimizu, M.; Takagaki, Y.
J. Immunol. 155, 1981-1993, 1995
A;Title: Diversity of T cell receptor delta-chain cDNA in the thymus of a one-month-old A;Accession: 146626
A;Accession: 146626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Molecule type: DNA
A,Residues: 1-118 <CAT>
A,Residues: 1-118 <CAT
A,Note: this sequence was determined from the germline gene
A,Note: this sequence was determined from a hybridoma protein that binds influenza virus l
C,Superfamily: immunoglobulin V region; immunoglobulin homology
C,Reywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E27889

Ig heavy chain V region (H18-S415) - mouse

Ig heavy chain V region (H18-S415) - mouse

Ig heavy chain V region (H18-S415) - mouse

C,Species in mesculus (house mouse)

C,Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996

C,Accession: E27889

R,Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.

EMBO J. 5, 1577-1587, 1986

A,Title: Structural and functional implications of a restricted antibody response to a A,Reference number: A91043; MUID:86300658; PMID:2427335
                                                                                                                                                                                                                                                                                                                                                                                                                              58 PWELATAPDVRISWRRG--HFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNL 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : | | : | : | : | : : : | 56 VSWVRQAPGKGLEWVAGITDSGGSTYYA---PAVK----GRFTISRNNGQSTATLQMNSL 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116 QKQDQSVYFCRVEL--DTRSSGRQQWQSIEGTKLSITQGQQRTKATTPAREPFQNT-EEP 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87 PSI----HKDYVNRLFLNWTEGQKSGFLRISNLQKQDQSVYFCRVELDTRSS-----GRQ 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53 DDINYTYYSDSVKGRFTISRDNAKONYLQLSSLKSBDTAMYYC----TRGSYYYDYGMD 107
                                                                                                                                                                                                                                                                     5 LLLPLLPLLLPPAPLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVBI------PPSPYY 57
                                                                                                                                                                                                                                                                                                                                                  LILLAAVPGLRAAATLDESGG-----GLVSP-----GGSLTLVCKGSGPTFSSYG 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 GVTQPKHLSASMGGSVE-----IPFSFYYPWELATAPDVRISWRRGHFHGQSFYSTRP 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 GLVKP------GGSLKLSCAASGITFSDYYMYWQTPDKRLEW------VATIT 52
                                                                                                                                                                                             Gaps
                                                                                                                                                                                             45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40;
                                                                                                                    Length 572;
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                                                                                                                                                                                             91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            173 YENIRNEGONTDPKLNPKDDGIVYASLALSSSTSPRAPPSH 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    167 VVGCLATGYIPGP-----VTPSWSGASGATSVTVPETH 199
                                                                                                                DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 8.3%; Score 101; DB 2; Best Local Similarity 24.8%; Pred. No. 0.14; Matches 33; Conservative 25; Mismatches 35
                                                                                                            8.5%; Score 104.5; DE 22.2%; Pred. No. 0.51;
                                                                                                                                                                                         36; Mismatches
C,Keywords: immunoglobulin
F;37-120/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             108 YWG--QGTSVTVS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     138 QWQSIEGTKLSIT 150
                                                                                                                                                                                         49, Conservative
                                                                                                                                                    Best Local Similarity
Matches 49; Conserve
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                                                                                                                Query Match
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                          OM protein - protein search, using sw model
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Run on:

December 23, 2005, 20:19:13 ; Search time 99.2506 Seconds (without alignments) 1634.967 Million cell updates/sec

Title: Perfect score: Sequence:

US-10-780-043-4 1223 1 MGRPLLLPLLPLLPPAFLQ......PSHRPLKSPQNETLYSVLKA 230

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2166443 seqs, 705528306 residues Searched:

2166443 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SIMMARIES

	Description	Ogukil homo sapien	homod	homo		Q5w434 brachydanio	Q5w433 brachydanio	Q9bzz2 homo sapien	Q8tbc9 homo sapien	Q58de8 bos taurus	Q62230 mus musculu	Q7yrq7 sus scrofa	Q4t054 tetraodon n	Q9jme9 mus musculu	Q96dn8 homo sapien	Q5tyr7 homo sapien	Q96rw7 homo sapien	Q4t853 tetraodon n	homo	Q9hbs0 homo sapien	homod	Q6piq7 homo sapien	Q501v7 brachydanio	Q5i0jl rattus norv	Q6p2j1 homo sapien	Q516u6 chlamydophi	Q8bs24 mus musculu	Q6uxg0 homo sapien	Q7yrf5 canis famil	Q7m048 rattus norv	P70255 mus musculu	Q5w431 fugu rubrip
SB		AN SAN	A.N	AN	SE	RE	RE		AN	NI			NG	SB	AN	AN	AN	ŊĠ	AN	AN	2	AN	RB		AN	AB	SE	AN	FA			RU
SUMMARIES	ID	O9UKJ1 HUMAN	OBNHI1 HUMAN	Q9UKJO HUMAN	QBBYA6 MOUSE	QSW434 BRARE	Q5W433_BRARE	SN HUMAN	Q8TBC9 HUMAN	Q58DE8_BOVIN	SN MOUSE	Q7YRQ7 PIG	Q4T054 TETNG	Q9JME9 MOU	Q96DN8 HUMAN	Q5TYR7 HUMAN	Q96RW7_HUMAN	Q4T853 TETNG	Q69YF9_HUM	Q9HBS0_HUMAN	SIGLS HUMAN	Q6PIQ7_HUM	Q501V7_BRARE	Q5I0J1_RAT	Q6P2J1_HUM	OSLEUG CHL	Q8BS24 MOUSE	QEUXGO HUM	Q7YRF5 CANFA	Q7M048 RAT	NFIC MOUSE	QSW431 FUGRU
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	Query Match	96.0	85.4	60.8	41.3	10.3	10.3	9.3	9.1	9.0	8.9	8.9	8.7	8.5	8.5	8.5	8.5	8.5	8.4	8.4	8.4	8.3	8.3	8.3	8.1	8.1	8.1	8.0	8.0	8.0	8.0	8.0
	Score	1173.5	1044	744	505.5	126	126	113.5	111.5	109.5	109	109	106	104	104	104	104	103.5	102.5	102.5	102.5	102	102	101	99.5	99.5	99.5	86	86	97.5	97.5	97.5
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QSw436 fugu rubrip QSw435 fugu rubrip										P11912 homo sapien
QSW436 FUGRU QSW435 FUGRU	P70232 MOUSE VPRE1_MOUSE	Q5W1K4_MOUSE Q545E0_MOUSE	Q6ZVX0_HUMAN	OFPJGO HUMAN	Q99M11_MOUSE	070188_RAT	Q7TMK4_MOUSE	Q10465_HUMAN	Q8WZ42 HUMAN	CD79A_HUMAN
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33	34 35	36 37	38	33	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 Ogukal HUMAN PRELIMINARY; PRT; 303 AA. AC OGUKALI HUMAN PRELIMINARY; PRT; 303 AA. AC OGUKALI HUMAN PRELIMINARY; PRT; 303 AA. AC OGUKALI HUMAN PRELIMINARY; PRT; 303 AA. DT 01-MAX-2000 (TTEMBLEE]. 13, Last sequence update) BY INTERPROPER, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae; OC NGEL TaxID=9606; RN [1] NUCLEACTION SEQUENCE RN MEDLINE=20127940; PubMed=10660620; DOI=10.1074/jbc.275.6.4467; BRABL; APRIGOROUGHEST44; Home sapiens. BRABL; APRIGOROUGHEST44; Home sapiens. BRABC; GO:0007171; P:transmembrane receptor protein tyrosine kin; ISS. BRABC; SMO0409; IG; 1. BRA	95.0%; Score 11/3.5; UB 2; Length Similarity 75.6%; Pred. No. 7.7e-91; 9; Conservative 1; Mismatches 0; Indels	Qy 1 MGRPLLLPLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60	QY 61 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTGGQKSGFLRISNLQKQDQ 120 Db 61 LATAPDVRISWRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTGGQKSGFLRISNLQKQDQ 120	QY 121 SVYPCRVELDTRSGRQQMQSIEGTKLSITQ	Qy 152GORTKATTPAREPFO 167
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Q9UKJO HUMAN PRELIMINARY;
Q9UKJO;
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QBBYA6;
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Matches 140; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
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121
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AC QBBYA6;
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A Leschul S. Feingold E.A., Grouse L.H., Darge J.G.,

A Laschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhar N.K.,

A Laschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhar N.K.,

A Distchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,

Brownstein M.J., Usdin T.B., Toohlyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Usdin T.B., Toohlyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brohards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

N. Halton D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Racha S., Halton B.K., Ketreman M., Madan A., Rodrigues S., Sanchez A.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Radiguez A.C., Garriwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Kracyvinski M.I., Skalska U., Smailus D.B.,

Butterfield Y.S.N., Kracyvinski M.I., Skalska U., Smailus D.B.,

Butterfield Y.S.N., Kracyvinski M.I., Skalska U., Smailus D.B.,

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                       241 NTEEPYENIRNEGONTDPKLNPKDDGIVYASLALSSSTSPKAPPSHRPLKSPONETLYSV 300
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NTEEPYENIRNEGQNTDPKLNPKDDGIVYASLALSSSTSPRAPPSHRPLKSPQNETLYSV 227
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                                                                                                                                                                                                                                                                                                                                                                                                  PILRA protein.
Homo sapiens (Human).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia, Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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Straubberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, BC017812; AAH17812.1; -; mRNA.
InterPro; IPR001559; Ig.
InterPro; IPR007110; Ig-like.
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PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin domain.
SEQUENCE 226 AA; 25479 MW; 5938181797733A30 CRC64;
                                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sci. U.S.A. 99:16899-16903 (2002)
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01-OCT-2002 (TrEMBLrel. 22,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                         QBINII HUMAN PRELIMINARY,
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                                                                                              228 LKA 230
                                                                                                                                                   LKA 303
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168
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SVYPCRVELDTRSSGRQQWQSIEGTKLSITQGQQRTKATTPAREPFQNTESPYENIRNEG 180
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BMBL; AF161081; AAD52965.1; -; mRNA.
EMBL; AG134336; CAH10711.1; -; mRNA.
INTACt; Q9UXJ0; -.
GO; GO:0005515; F: procein binding; IPI.
GO; GO:0005515; F: procein binding; IPI.
GO; GO:0007171; P: transmembrane receptor protein tyrosine kin. . .; NAS.
INTERPRO; IPR003599; IG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20127940; PubMed=10660620; DOI=10.1074/jbc.275.6.4467; Mousseau D.D., Banville D., L'Abbe D., Bouchard P., Shen S.H.; "PILRalpha, a novel immunoreceptor tyrosine-based inhibitory motif-bearing protein, recruits SHP-1 upon tyrosine phosphorylation and is jaired with the truncated counterpart PILRabeta."; J. Biol. Chem. 275:4467-4474(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-FBA-2005 (TrEMBLrel. 29, Last annotation update)
Activating receptor PilRbeta (Hypothetical protein DKFZp4340079)
Name=DKFZp4340079;
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86.4%; Pred. No. 1.1e-54;
tive 7; Mismatches 15; Indels
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Hypothetical protein; Immunoglobulin domain; Receptor.
SEQUENCE 227 AA; 25542 MW; 7FF960C60AB7EF09 CRC64;
                                                                                                                                              ONTOPKLNPKDDGIVYASLALSSSTSPRAPPSHRPL
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Sequence 4, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 8, Appli
Sequence 10, Appl
Sequence 485, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 754, Appli
Sequence 77, Appli
Sequence 77, Appli
Sequence 22, Appli
Sequence 24, Appli
Sequence 22, Appli
Sequence 22, Appli
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Sequence 32, Appl
Sequence 7589, Ap
                                                                                         December 23, 2005, 20:20:23 ; Search time 23.9707 Seconds (without alignments) 793.277 Million cell updates/sec
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(cgn2_6/ptodata/1/iaa/RE COMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-956-2
US-09-546-049-2
US-09-869-388-8
US-09-869-388-8
US-09-869-388-10
US-09-149-476-485
US-09-869-388-10
US-09-149-476-754
US-09-149-476-754
US-09-149-016-10503
US-09-149-016-10503
US-09-149-016-10503
US-08-918-148-77
US-08-918-148-77
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US-08-918-148-77
US-08-918-146-22
US-08-97-146-22
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Maximum Match 100%
Listing first 45 summaries
                                                            OM protein - protein search, using sw model
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Sequence 7590, Ap Sequence 5, Appli Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 213, App	AND RELATED COMPOSITIONS AND	Length 230; Indels
2 US-09-949-016-7590 2 US-08-759-628-5 1 US-08-61-052-16 2 US-09-188-082-16 2 US-09-102-716-16 2 US-09-905-715A-213 2 US-09-905-775A-213 2 US-09-905-775A-213 2 US-09-906-775A-213 2 US-09-906-700-213 2 US-09-906-713-13 2 US-09-906-64-213 2 US-09-906-646-213	ALIGNMENTS 9869388 11e 8-DERIVED NUCLEIC ACIDS US/09/869,388	Score 1223; DB 2; Pred. No. 3e-110; 0; Mismatches 0; APSGSTGSGPSYLYGYTQPKHL LQPSGSTGSGPSYLYGYTQPKHL LQPSGSTGSGPSYLYGYTQPKHL LQPSGSTGSGPSYLYGYTQPKHL APSGSTGSGPSYLYGYNRLFLNW SETSTRPPSIHKDYVNRLFLNW ACSIGTKLSITQGQRTKATTP L
2.1.8 2.1.8	ULT 1 09-869-188-4 atent No. 6774214 atent No. 6774214 ENERAL INFORMATION: ENERAL INFORMATION: APPLICANT: Bates, Elizabeth APPLICANT: Cournier, Nathalie APPLICANT: Cournier, Nathalie APPLICANT: Garrone, Pierre TITLE OF INVENTION: MONOCYTE-DERIV FILE REPRERICE: SF0997X CURRENT APPLICATION NUMBER: US/09/ CURRENT PILING DATE: 2002-02-21 NUMBER OF SEQ ID NOS: 14 ESNGTH: 230 TYPE: PRT OGGANISM: homo sapiens	ch Similarity 100.0%; 230; Conservative 1 MGRPLILPLPLLIPPAET 1 MGRPLILPLPLLPPAET 1 MGRPLILPLPLLPLPPAET 1 MGRPLILPLPLLPPAET 2 LATAPDVRISWRRGHFHGG 61 LATAPDVRISWRRGHFHGG 61 LATAPDVRISWRRGHFHGG 62 LATAPDVRISWRRGHFHGG 63 LATAPDVRISWRRGHFHGG 64 LATAPDVRISWRRGHFHGG 65 LATAPDVRISWRRGHFHGG 66 LATAPDVRISWRRGHFHGG 72 SVYFCRVELDTRSSGRQOV 73 SVYFCRVELDTRSSGRQOV 74 SVYFCRVELDTRSSGRQOV 75 SVYFCRVELDTRSSGRQOV 76 LATAPPRICATION: 76 A 6 0076 76 LATAPPRICATION: 76 A 6 0076 76 LATAPPRICATION: 76 A 6 0076 76 COF LINVENTION: 76 TO SEQUENCES: 22
22223333333333333333333333333333333333	RESULT 1 US-09-869-388-4 ; Sequence 4, Applicat ; Patent No. 6774214 ; GENERAL INFORMATION: ; APPLICANT: Bates, E APPLICANT: Fournie ; APPLICANT: Garrone ; APPLICANT: Garrone ; TITLE OF INVENTION: ; FILE REFERENCE: SFO ; CURRENT APPLICATION ; FILE REFERENCE: SFO ; CURRENT APPLICATION ; SOFTWARE: IBM PC CO ; SEQ ID NO 4 ; LENGTH: 230 ; TYPE: PRT ORGANISM: homo sap US-09-869-388-4	Query Match Best Local Similarity Matches 230; Conservat C

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SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: California
                                                                  Meyaard,
                               APPLICANT: Adema,
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                               S: DNAX Research Institute
901 California Avenue
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108-09-546-049-2
1 Sequence 2, Application US/09546049
1 Patent No. 6479638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (650) 496-1204
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TYPE: amino acid
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Best Local Similarity 75.9
Matches 230; Conservative
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CORRESPONDENCE ADDRESS
                                                                                        CITY: Palo Alto
STATE: California
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STREET: 90
                                                                                                                                                  COUNTRY:
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240 LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQ 120 167 168 NTEEPYENIRNEGONTOPKLAPKODGIVYASLALSSSTSPRAPPSHRPLKSPONETLYSV 227 .----- 151 9 1 MGRPLLLPLLPLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 181 TOGKRRSDSWHISLETAVGVAVAVTVLGIMILGLICLLRWRRRKGÖÖRTKATTPAREPFÖ 1 MGRPLLLPLLPLLPPAFLQPSGSTGSGPSYLYGVTQPXHLSASMGGSVEIPFSFYYPWE Gaps 73; Lanier, Lewis L.
Phillips Jr., Joseph H.
TITLE OF INVENTION: Isolated Mammalian Monocyte Cell Genes;
NUMBER OF SEQUENCES: 22 DB 2; Length 303; 121 SVYFCRVELDTRSSGRQQWQSIEGTKLSITQ--------0; Indels COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION WHERE: US/09/546,049
FILING DATE: 10-Apr-2000
PRIOR APPLICATION DATA: ..4e-105; APPLICATION NUMBER: US/08/985,950
FILING DATE: 05-DEC-1997
APPLICATION NUMBER: US 60/041,279
FILING DATE: 21-MARCH-1997
APPLICATION NUMBER: US 60/033,181
FILING DATE: 16-DEC-1996
APPLICATION NUMBER: US 60/032,252
FILING DATE: 06-DEC-1996
ATTORNEY/AGENT INFORMATION: ADDRESSEE: DNAX Research Institute STREET: 901 California Avenue CITY: Palo Alto Query Match
96.2%; Score 1176.5;
Best Local Similarity 75.9%; Pred. No. 1.4e
Matches 230; Conservative 0; Mismatches NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REPERENCE/DOCKET NUMBER: DX0670K
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196 TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-546-049-2 Gorman, Daniel M. McClanahan, Terrill K. Zurawski, Sandra M. Zurawski, Gerard COUNTRY: USA ZIP: 94304-1104 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk LENGTH: 303 amino acids TYPE: amino acid Gosse Jan 윱 δ

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December 23, 2005, 20:40:10 ; Search time 78.2515 Seconds (without alignments) 1228.101 Million cell updates/sec
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1223
1 MGRPLLLPLLPLLPPAFLQ......PSHRPLKSPQNETLYSVLKA 230
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  5.1.6
Compugen Ltd
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GenCore version
Copyright (c) 1993 - 2005
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Maximum Match 100%
Listing first 45 summaries
                                                                             OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                                                                                                                  Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Published Applications ÂA Main:*

1. /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2. /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

3. /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

4. /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*

5. /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*

5. /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*

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Database :

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	Description	Sequence	Sequence	Sequence				/Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
SUMMARIES	aı	US-10-780-043-4	US-10-309-290-010-10-	- _	US-10-290-631-2 (AUM)	US-10-780-043-2	US-10-777-524-2 (ALC " 1	١.		US-10-450-763-30868	US-10-450-763-33210	US-10-450-763-47228	US-10-450-763-51762	US-10-780-043-8	US-09-745-763-106	US-09-774-381-44	-10-780-043	US-09-809-391-485	US-09-882-171-485	US-10-164-861-485	US-10-262-445-128	US-10-780-043-6		US-09-935-390A-21	US-10-276-774-2380	US-09-809-391-754	US-09-882-171-754	US-10-164-861-754
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ouerv	_ !	100.0	9.66	96.2	96.2	96.2	96.2	96.2	86.4	67.9	67.9	67.9	67.9	66.7	62.6	62.1	62.1	6.09	60.9	60.9	60.8	60.8	60.8		60.8	42.3	42.3	42.3
	Score	1223	1218	1176.5	1176.5	1176.5	1176.5	1176.5	1057	830	830	830	830	816	765	759	759	745	745	745	744	744	744	744	744	517	517	517
Result	No.	7	7	m	4	Ŋ	9	7	89	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27

Sequence 711, App	Sequence 4, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 92, Appl	Sequence 184, App	Sequence 158, App	Sequence 24, Appl	168,	Sequence 174, App	Seguence 18, Appl	Sequence 36, Appl	Sequence 51, Appl	Sequence 51, Appl	Sequence 58, Appl	09	Sequence 35, Appl	Sequence 1562, Ap
US-09-866-050A-711	US-10-290-631-4	US-10-777-524-4	US-10-777-521-4	US-10-788-625-92	US-10-479-670-184	US-10-479-670-158	US-09-863-776-24	US-10-479-670-168	US-10-479-670-174	US-10-779-461-18	US-10-203-708-36	US-09-870-759-51	US-09-751-708A-51	US-09-863-776-58	US-09-863-776-60	US-10-203-708-35	US-10-408-765A-1562
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224	66	66	66	124	253	247	1700	252	253	253	1694	1709	1709	1709	1709	1709	1709
28.9	18.2	18.2	18.2	6.6	9.5	9.4	4.6	9.4	9.4	9.4	9.3	9.3	9.3	9.3	9.3	9.3	9.3
354	222	222	222	120.5	116.5	115.5	115.5	114.5	114.5	114.5	113.5	113.5	113.5	113.5	113.5	113.5	113.5
28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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APPLICANT: Bates, Elizabeth
APPLICANT: Bates, Elizabeth
APPLICANT: Bates, Elizabeth
APPLICANT: Chalus, Lional
APPLICANT: Chalus, Lional
APPLICANT: Chalus, Lional
APPLICANT: Garrone, Pierre
TITLE OF INVENTION: MONOCYTE-DERIVED NUCLEIC ACIDS AND RELATED COMPOSITIONS AND METH
FILER REFERENCE: SF0977X
CURRENT APPLICATION NUMBER: US/10/780,043
CURRENT PILING DATE: 2004-02-17
PRIOR PILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: IBM PC compatible
SEQ ID NO 4
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Sequence 110, Application US/10309290

Publication No. US-20040023241A1

GENERAL INFORMATION:
APPLICANT: Algobrook II, John P.
           ; Sequence 4, Application US/10780043; Publication No. US20040137506A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 230; Conservative
                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: homo sapiens
US-10-780-043-4
                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 230
US-10-780-043-4
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APPLICANT: MOLGEATHY, Sean A.
APPLICANT: MOLGEATHY, Sean A.
APPLICANT: Pan, Yang
APPLICANT: Pan, Yang
APPLICANT: Pan, Yang
APPLICANT: Gearing, David P.
TITLE OF INVENTION: NOVEL BIRR, WTR-1, LSP-1, TAP-1, AND PA-1 MOLECULES
FILE REPERENCE: MNI-107CP2
CURRENT APPLICATION NUMBER: US/09/774,381
CURRENT APPLICATION NUMBER: 08/941,354
PRIOR PILING DATE: 1999-09-30
PRIOR PILING DATE: 1999-09-30
PRIOR PILING DATE: 1998-01-27
PRIOR PILING DATE: 1998-01-27
PRIOR APPLICATION NUMBER: 09/014,347
PRIOR FILING DATE: 1999-10-06
PRIOR FILING DATE: 1998-01-06
PRIOR PILING DATE: 1998-01-06
PRIOR FILING DATE: 1997-10-06
PRIOR PILING DATE: 1997-10-10-14
PRIOR PILING DATE: 1998-10-10-14
PRIOR PILING DATE: 1997-10-10-14
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121 SVYFCRVELDTRSSGRQQWQSIEGTKLSITQGQQRTKATTPAREPFQNTEEPYENIRNEG 180
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                                                                        181 QNTDPKLNPKDDGIVYASLALSSSTSPRAPPSHRPLKSPQNETLYSVLKA 230
                                                                                                                          181 ONTDPKLNPKDDGIVYASLALSSSTSPRAPPSHRPLKSPONEMLYSVLKA 230
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96.2%; Score 1176.5; DB 3; Length 303;
Best Local Similarity 75.9%; Pred. No. 5.3e-96;
Matches 230; Conservative 0; Mismatches 0; Indels 73;
                                                                                                                                                                                                                                                                                                                             Sequence 58, Application US/09774381 Publication No. US20030082677A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                Holtzman, Douglas A
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ORGANISM: Homo mapienm
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CURRENT APPLICATION NUMBER: US/10/309,290

CURRENT PILING DATE: 2002-12-02

PRIOR PELING DATE: 2001-12-05

PRIOR PELING DATE: 2001-12-05

PRIOR PELING DATE: 2001-12-05

PRIOR PELING DATE: 2001-12-07

PRIOR PELING DATE: 2001-12-17

PRIOR APPLICATION NUMBER: 60/341,477

PRIOR PELING DATE: 2001-12-17

PRIOR PELING DATE: 2001-12-31

PRIOR PELING DATE: 2001-12-31

PRIOR PELING DATE: 2001-12-31

PRIOR PELING DATE: 2002-04-17

PRIOR PELING DATE: 2002-04-17

PRIOR PELING DATE: 2002-05-15

PRIOR PELING DATE: 2002-05-15
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99.6%; Score 1218; DB 4; Length 230;
Best Local Similarity 99.6%; Pred. No. 7.7e-100;
Matches 229; Conservative 0; Mismatches 1; Indels
                      Boldog, Ferenc L.
Burgess, Catherine E.
Chillakuru, Rajeev A.
Edinger, Shlomit R.
Gerlach, Valerie L.
Gorman, Linda
Gould-Rotherg, Bonnie E
                                                                                                                                                                                                                                                                                                                                                                                                                                Malyankar, Uriel M.
Miller, Charles E.
Murphey, Ryan
Patturajan, Mera
Peyman, John A.
Rastelli, Luca
Rieger, Daniel K.
Shency, Suresh G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Smithson, Glennda
Starling, Gary
Taupier, Raymond J.
Voss, Edward Z.
                                                                                                                                                                                                                                                                                                                             Michael B.
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Zhong, Mei
                                                                                                                                                                                                                                                                                           Guo, Xiaojia
Jeffers, Mich
                                                                                                                                                                                                                                                                                                                                                                   Ji, Weizhen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) ORGANISM: Homo sapiens
U8-10-309-290-110
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2077, Ap
2079, Ap
907, App
27, Appl
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                                                                        December 23, 2005, 20:41:30 ; Search time 4.35831 Seconds (without alignments) 376.418 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                      1 MGRPLLLPLLPLLPPAFLQ......PSHRPLKSPQNBTLYSVLKA 230
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                                                                                                                                                                                                                                                                                                                                                             Published Applications AA New:*

1: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*
 5.1.6
Compugen Ltd.
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US-11-135-855-35
US-10-512-184-62
US-10-512-184-64
US-10-512-184-64
US-10-512-184-65
US-10-512-184-65
US-10-512-184-65
US-11-054-515-2079
US-11-054-515-2079
US-11-054-515-2079
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                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
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GenCore version
Copyright (c) 1993 - 2005
                                                                                                                                                                                                                     54001 segs, 7132810 residues
                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                 - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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1223
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1113.5
1112.5
1112.5
1112.5
1112.5
1110.5
100.5
100.5
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102.5
102.5
102.5
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                                                                                                                                                                                                                                                                      Minimum DB
Maximum DB
                                                 OM protein
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Sequence Seq	Sequence
US-11-054-515-1787 US-11-054-515-1884 US-11-054-515-1884 US-11-054-515-1525 US-11-054-515-1080 US-11-054-515-1080 US-11-054-515-1081 US-11-054-515-1083 US-11-054-515-1083 US-11-054-515-1083 US-11-054-515-1083 US-11-054-515-868 US-11-054-515-868 US-11-054-515-868 US-11-054-515-868 US-11-054-515-868 US-11-054-515-868 US-11-054-515-868 US-11-054-515-868	US-11-054-515-1064
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1001.5 1000.5 10	0 0
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ALIGNMENTS

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US-10-995-561-974

Sequence 974, Application US/10995561

Sequence 974, Application US/10995561

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCIAL DISORDERS AND DRUG RESPONSE,
TITLE OF INVENTION: DETECTION AND USES THEREOF

FILE REPERENCE: CLOOIS59
CURRENT APPLICATION NUMBER: US/10/995,561

CURRENT PILLING DATE: 2004-11-24

NUMBER OF SEQ ID NOS: 85702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58 IWYY-DYSGQRQVVSHSADPKLVBARFRGRIEFMGNPEHRVCNLL-LKDLQPEDSGSYNF 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 RVELDTRSSGRQQWQSIEGTKLSITQGQQRTKATTPAREPFQNTE-----EPY----EN 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 SWRRGHFHGQS---FYSTRPPSIHKDYVNRL-FLNWTEGQKSGFLRISNLQKQDQSVYFC 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 LPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWELATAPDVRI
                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                          27;
                                                                                                                                                                                                                                                                                                                                                                                     DB 6; Length 1649;
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                                                                                                                                                                                                                                                                                                                                                                 Query Match 9.3%; Score 113.5; DB 6;
Best Local Similarity 24.2%; Pred. No. 0.021;
                                                                                                                                                                                                                                                                                                                                                                                                                        32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            171 VRLOWOGODP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    176 IRNEGONTOP 185
                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
US-10-995-561-974
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RESULT. 2
US-11-135-855-36

Sequence 36, Application US/11135855

Publication No. US20050255557A1

BEBREAL INFORMATION:
APPLICANT: SMITHKLINE BEECHAM CORPORATION
APPLICANT: SMITHKLINE BEECHAM p.l.c.

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126 RVELDTRSSGROOMOSIEGTKLSITOGOORTKATTPAREPPONTE-----EPY----EN 175
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                                                                                                                                                                                                                                171 VRLQWQGQDP 180
                                                                                                                                                                              176 IRNEGONTOP 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
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Publication No. US20050272054A1

GRNERAL INFORMATION:

APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GRNETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: DETECTION AND USES THEREOF

FILE REFERENCE: CLO1559

CURRENT PILING DATE: 2004-11-24

NUMBER OF SEQ ID NOS: 85702

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 9730
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 LPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWELATAPDVRI 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 LPKLLLLASFFPAGGAS-----WGVSSPQDVQGVKGSCLLIPCIFSFPADVEVPDGITA 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 LPKLLLLASFFPAGGAS-----MGVSSPQDVQGVKGSCLLIPCIFSFPADVBVPDGITA
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9.3%; Score 113.5; DB 7; Length 1
Best Local Similarity 24.2%; Pred. No. 0.021;
Matches 46; Conservative 32; Mismatches 85; Indels
FILE REFERENCE: GP50013
CURRENT APPLICATION NUMBER: US/11/135,855
CURRENT FILING DATE: 2005-05-24
PRIOR APPLICATION NUMBER: US/10/203,708
PRIOR FILING DATE: 2002-08-13
PRIOR FILING DATE: 2001-02-14
PRIOR FILING DATE: 2000-02-14
PRIOR FILING DATE: 2000-02-14
PRIOR FILING DATE: 2000-02-14
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-02-05
NUMBER OF SEQ ID NOS: 46
LENGTHARE: F8545EQ for Windows Version 3.0
SEQ ID NO 36
LENGTH: 1694
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171 VRLQWQGQDP 180
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ORGANISM: Homo sapiens
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US-11-135-855-36
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US-10-995-561-973
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Sequence 26. Application US/10512184

| Sequence 26. Application No. US20050244901A1
| Publication No. US20050244901A1
| GENERAL INFORMATION:
| APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.
| TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
| TITLE OF INVENTION: Antibodies, recombinant and fusions mediated plant disease
| TITLE OF INVENTION: Antibodies, resistance against fungi
| TITLE OF INVENTION: Antibodies, resistance against fungi
| TITLE OF INVENTION: Antibodies, resistance against fungi
| CURRENT APPLICATION NUMBER: US/10/512,184
| CURRENT FILING DATE: 2004-10-22
| NUMBER OF SEQ ID NOS: 72
| SOFTWARE: Patentin Ver. 2.1
| SEQ ID NO 26
| LENGTH: 258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 RVELDTRSSGROOWOSIEGTKLSITQGQQRTKATTPAREPPQNTE-----EPY----EN 175
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9.3%; Score 113.5; DB 7;
Best Local Similarity 24.2%; Pred. No. 0.022;
Matches 46; Conservative 32; Mismatches 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OS-11-135-855-95
OS-11-135-85-95
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OS-11-135-85
OS-11-135-85
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5.1.6 Compugen Ltd. GenCore version Copyright (c) 1993 - 2005

OM protein - protein search, using sw model

December 23, 2005, 20:18:33 ; Search time 126.054 Seconds (without alignments) 1056.147 Million cell updates/sec Run on:

US-10-780-043-2

Perfect score:

1591 1 MGRPLLLPLLPLLPPAFLQ.......PSHRPLKSPQNBTLYSVLKA 303 Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

2443163 segs, 439378781 residues Searched:

2443163 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

A_Geneseq_21:*

geneseqp1980s:*

geneseqp1990s: *
geneseqp2000s: *
geneseqp2002s: *
geneseqp2003s: *
geneseqp2003s: *
geneseqp2003s: *
geneseqp2004s: * 4.0.0.0

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Aaw62772 Human imm	Aab07443 A human m	Adp25129 PRO polyp		Ade95578 Human NOV	Ade95580 Human NOV	Aay08015 Human LSP	Aab07447 A human m	Aaw80407 A secrete	Abp61825 Human pol		Abu89824 INF-recep	Aaw63682 Human sec			Human	Abo34539 Region of		Adh74202 Human sec	Adk98565 Human imm	Aab07446 A human m	Abg00509 Novel hum	Abg16869 Novel hum	Abg02851 Novel hum
SUMMARIES		ΩI	AAW62772	AAB07443	ADP25129	AAB07444	ADE95578	ADE95580	AAY08015	AAB07447	AAW80407	ABP61825	AAB07445	ABU89824	AAW63682	ABB12010	AAY87230	ABG95345	AB034539	AD123200	ADH74202	ADK98565	AAB07446	ABG00509	ABG16869	ABG02851
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	Query	Match	100.0	100.0	8.66	73.9	73.6	63.5	61.2	61.2	60.8	8.09	60.2	60.2	60.2	60.2	59.4	58.7	58.7	58.7	58.7	58.3	51.6	50.8	50.8	50.8
		Score		1591	1588	1176.5	1171.5	1010.5	973.5	973.5	967.5	967.5	958	958	958	958	945	934	934	934	934	927.5	821	808	808	808
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ALIGNMENTS

AAW62772

AAW62772 standard; protein; 303 AA

AAW62772;

23-SEP-1998 (first entry)

Human immunoglobulin receptor designated FDF03

Human; type I transmembrane protein; immunoglobulin-like domain; FDF03; activated monocyte; YE01; KTE03; control; development; differentiation; mammalian immune system; treatment; cancerous condition; degenerative condition; autoimmune response; transplantation rejection; graft versus host disease; inflammatory condition; detection; diagnosis; drug screening.

C WO9824906-AZ. Homo sapiens.

11-JUN-1996

97WO-US021101.

05-DEC-1997;

96US-0032252P. 96US-00762187. 96US-0033181P. 97US-0041279P. 09-DEC-1996; 16-DEC-1996; 21-MAR-1997; 06-DEC-1996;

(SCHE) SCHERING CORP.

Zurawski SM; Gorman DM, Mcclanahan TK, Phillips JH; Meyaard L, G Adema GJ, Me Zurawski G,

WPI; 1998-333325/29. N-PSDB; AAV38987.

New isolated activated monocyte cell gene(s) - used to develop products for treating e.g. cancer, degenerative conditions, autoimmune responses, transplant rejection or inflammatory conditions.

Claim 1; Page 60-61; 104pp; English.

The present sequence represents a human protein, FDF03, which is a type I transmembrane protein comprising an extracellular portion characterised by immunoglobulin-like domains, indicating that the protein is a receptor

us-10-780-043-2.rag

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(SCHE ) SCHERING CORP
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member of the immunoglobulin superfamily. The FDF03 gene is found in activated monocytes. The specification also describes other proteins encoded by activated monocytes, which are designated YED1 and KTE03. The genes function in controlling development, differentiation, and/or treating abnormal proliferation, regeneration, degeneration or atrophy. They can be used for treating e.g. cancerous conditions, degenerative conditions, autoimmune responses, transplantation rejection, graft versus host disease, or inflammatory conditions. The products can also be used for detection, diagnosis and drug screening
                                                                                                                                                                                                                    LATAPDVRISWRRGHFHGQSPYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQ 120
                                                                                                                                                                                                                                    LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQ 120
                                                                                                                                                                                                                                                                                                    TQGKRRSDSWHISLETAVGVAVAVTVLGIMILGLICLLRWRRRKGQQRTKATTPAREPFQ 240
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                                                                                                                                                                                                                                                                                                                                                       SVYPCRVELDTRSSGROOWQSIEGTKLSITQAVTTTTORPSSMTTTWRLSSTTTTTGLRV 180
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                                                                                                                                                                                               1 MGRPLLLPLLPLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPPSFYYPWE 60
                                                                                                                                                                            MGRPLLLPLLPLLPLEPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVBIPFSFYYPWE
                                                                                                                                                          Gaps
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FDF03-M14, FDF03-S2; haematopoietic cell; monocyte hyperplasia;
tissue rejection; inflammation; infection.
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                                                                                                                                   100.0%; Score 1591; DB 2; Length 303; 100.0%; Pred. No. 7.7e-122; 1ve 0; Mismatches 0; Indels 0
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/note= "mature protein"

    19
    note= "signal peptide"

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98US-00224604
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                                                                                                                                             al Similarity 100.
303; Conservative
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                                                                                                                Sequence 303 AA;
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31-DEC-1998;
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Best Local
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The present sequence represents a human monocyte-derived protein. The specification describes monocyte-derived proteins FDF03, FDF03DeltaTM, PDF03.51. PDF03.51. PDF03.51. PDF03.51. The proteins are involved in the regulation, or development, of haematopoietic cells. Antibodies specific for antigenic components of the proteins can be used to detect the components in samples. The proteins can also be used to detect the candidate therapeutic agents. The monocyte-derived proteins and polynucleotides can be used for diagnosis of diseases related to an increase, or decrease, in the number of monocytes in a tissue or lymph system, such as monocyte hyperplasia, tissue or graft rejection, inflammation, or bacterial or viral infections. The proteins can also be used in the treatment of disorders associated with abnormal expression or
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                                                                                                                                                                 Novel monocyte-derived polypeptides and polynucleotides, used to diagnose diseases associated with changes in monocyte numbers, e.g. bacterial or viral infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQ 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MGRPLLLPLLLPLPLAPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 TQGKRRSDSWHISLETAVGVAVAVTVLGIMILGLICLLRWRRRKGQQRTKATTPAREPFQ
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; Pred. No. 7.7e-122;
0; Mismatches 0;
   Garrone P;
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                                                                                                                                                                                                                                                                                                Claim 1; Page 32-33; 45pp; English.
   Chaulus L,
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Matches 303; Conservative
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N-PSDB; AAA58814.
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Sequence 2, Appli
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                                                                                 December 23, 2005, 20:20:23 ; Search time 31.5788 Seconds (without alignments) 793.277 Million cell updates/sec
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1 MGRPLLLPLLPLLPPAFLQ......PSHRPLKSPQNETLYSVLKA 303
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(cgn2_6/ptodata/1/iaa/RE COMB.pep:*

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Compugen Ltd.
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 GenCore version (c) 1993 - 2005
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Sequence 39, Appl Sequence 39, Appl Sequence 39, Appl Sequence 6729, Appl Sequence 22, Appl Sequence 67, Appl Sequence 67, Appl Sequence 63, Appl Sequence 63, Appl Sequence 63, Appl Sequence 79, Appl Sequence 4, Appl Sequence 6, Appl Sequence 6	Genes ;	.h 303;
2 US-09-904-462-39 2 US-09-902-736A-39 2 US-09-906-722A-39 2 US-09-9010-66729 2 US-09-949-016-6729 1 US-08-597-495B-22 2 US-09-086-051A-22 2 US-09-086-051A-22 2 US-09-334-465A-6 2 US-09-334-465A-6 2 US-09-334-499-6 2 US-09-338-243D-13 2 US-09-338-243D-13 2 US-09-318-18-79 2 US-09-188-091A-77 1 US-08-661-052-4 2 US-09-188-082-4 2 US-09-188-082-4	ALIGNMENTS 08985950 (e Jan lated Mammalian Monocyte Cell lated Mammalian Monocyte Cell lask atible DOS/MS-DOS lease #1.0, Version #1.30 8/08/985,950 997 8 60/041,279 -1997 5 60/033,181 996 ON: 34,090 R: DX0670K ATION: 196 4 2:	100.0%; Score 1591; DB 2; Length 100.0%; Pred. No. 1.5e-141;
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	Dijcatic 0076 0076 0076 0076 0076 0076 0076 007	Similarity
28 29 30 31 31 32 33 34 34 35 36 37 37 37 38 39 40 40 41 41 40 41 41 40 41 40 40 41 40 40 40 40 40 40 40 40 40 40	RESULT 1 US-08-985-950-2 Sequence 2, ABD13 Sequence 2, ABD13 Sequence 2, ABD13 Sequence 2, ABD13 SEQUENCE NO. GIAGO GENERAL INVERNAT: A PAPLICANT: A PAPLICANT: Palo CONTRY: P	Query Match Best Local

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Gorman, Daniel M.
McClanahan, Terrill K.
Zurawski, Sandra M.
Zurawski, Gerard
Lanier, Lewis B.
Phillips Jr., Joseph H.
TITLE OF INVENTION: Isolated Mammalian Monocyte Cell Genes;
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COMPUTER: ELDOPY disk COMPUTER: TEM PC COMPUTER: PENDALE PORM: MEDIUM TYPE: Floppy disk COMPUTER: TEM PC COMPUTER: DATE: PC-DOS/MS-DOS SOFTWARE: PATENTING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTON NUMBER: US (09/95,950 FILING DATE: 10-Apr-2000 PRIOR APPLICATION NUMBER: US 60/041,279 FILING DATE: 16-DEC-1997 APPLICATION NUMBER: US 60/033,181 FILING DATE: 16-DEC-1996 ATTORNEY/AGENT INFORMATION: WARRET US 60/032,252 FILING DATE: 16-DEC-1996 ATTORNEY/AGENT INFORMATION:
0; Indels
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0670K
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Related Reagents
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Patent No. 6479638
GENERAL INFORMATION:
APPLICANT: Adema, Gosse Jan
303; Conservative
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Sequence 2, Application US/09869388

Sequence 2, Application US/09869388

Sequence 2, Application US/09869388

GENERAL INFORMATION:
APPLICANT: Bates, Elizabeth
APPLICANT: Fournier, Nathalie
APPLICANT: Chalus, Lionel
APPLICANT: Garrone, Pierre
APPLICANT: Garrone, Pierre
APPLICANT: Garrone, Pierre
APPLICANT: Garrone, NonCYTE-DERIVED NUCLEIC ACIDS AND RELATED COMPOSITIONS AND METHO
FILE REFERENCE: SF09777
CURRENT APPLICATION NUMBER: US/09/869,388
CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: IBM PC compatible
SEQ ID NO 2
IENGTH: 303
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Pred. No. 1.5e-141;
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MOLECULE TYPE: protein
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SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-546-049-2
                                            LENGTH: 303 amino acids
TYPE: amino acid
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Matches 303; Conservative 0
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS
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US-09-869-388-2
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December 23, 2005, 20:40:10 ; Search time 103.088 Seconds (without alignments) 1228.101 Million cell updates/sec
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1591
1 MGRPLLLPLLPLLPPAFLQ......PSHRPLKSPQNETLYSVLKA 303
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Listing first 45 summaries
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	Description	58 Sequence 58, Appl	2	7	Sequence 2, Appli	~	4	7	12 Sequence 112,	4 Sequence 44, 1	0 Sequence 10,	06 Sequence 106,	28 Seguence 128,	Sequence 6, A	7,	Sequence	80 Sequence 238	5 Sequence	Sequence	85 Sequence 485,	Seguence	Seguence	Sequence	7228 Sequence 47228,	762 Sequence	4 Sequence 754,	4	754
SUMMARIES	OI 1	US-09-774-381-	US-10-290-631-2	US-10-780-043-2	US-10-777-524-2	. US-10-777-521-2	US-10-780-043-4	US-10-309-290-1	US-10-309-290-1	US-09-774-381-4	US-10-780-043-1	US-09-745-763-1	US-10-262-445-1	US-10-780-043-6	US-10-820-474A-	US-09-935-390A-21	US-10-276-774-2380	US-09-809-391-48	US-09-882-171-4	US-10-164-861-4	US-10-780-043-8	. US-10-450-763-30868	. US-10-450-763-33210	. US-10-450-763-4	. US-10-450-763-51	US-09-809-391-75	US-09-882-171-75	US-10-164-861-7
	Query Match Length DB	303 3	303 4	303 4	303 4	303 5	230 4	230 4	206 4	226 3	226 4	226 3	227 4	227 4	227 5	291 3	326 4	238 3	238 3	238 4	175 4	1012 5	1012 5	1012 5	1012 5	101 3	101 3	101 4
de	Query Match	100.0	100.0	100.0	100.0	100.0	73.9	73.6	63.5	61.2	61.2	60.8	60.2	60.2	60.2	60.2	60.2	58.7	58.7	58.7	51.6	50.8	50.8	50.8	50.8	32.5	32.5	32.5
	Score	1591	1591	1591	1591	1591	1176.5	1171.5	1010.5	973.5	973.5	967.5	928	958	958	958	958	934	934	934	821	808	808	808	808	517	517	517
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Sequence 711, App Sequence 4, Appli Sequence 4, Appli Sequence 391, Appli Sequence 3, Appli Sequence 3, Appli Sequence 104, App Sequence 104, App Sequence 120, App Sequence 120, App Sequence 120, App Sequence 18, Appl Sequence 1	Sequence 18, Appl Sequence 40, Appl Sequence 40, Appl Sequence 40, Appl Sequence 40, Appl Sequence 40, Appl
US-09-866-050A-711 US-10-290-631-4 US-10-777-521-4 US-10-777-521-4 US-10-291-265-391 US-10-962-127-3 US-10-962-127-3 US-09-796-753-104 US-09-796-753-120 US-10-291-265-863 US-09-965-529-18	US-09-969-680A-18 US-10-227-884-40 US-10-230-163-40 US-10-230-338-40 US-10-218-631-40 US-10-230-414-40
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ALIGNMENTS

MOLECULES	Gaps
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AND PA-I	Length 303; Indels 0
TAP-1,	
	Score 1591; DB 3; Pred. No. 6.6e-126; Mismatches 0;
1 MTR-1, EFOR 354 354 149 159 143 414 414 890	ore 1591; ed. No. 6. Mismatches
on US/09774381 bouglas A. Sean A. David P. David P. David P. NOVEL EDIRF, MTR-1, AND USES THEREFOR 107672 107672 2001-01-30 BER: 08/041,354 999-03-09-30 BER: 09/010,674 999-01-20 BER: 09/014,347 998-01-27 998-01-27 998-01-27 BER: 09/01,159 997-10-06 BER: 09/014,347 BER: 09/014,347 BER: 09/011,159 997-10-06 BER: 09/014,347 BER: 09/011,151 BER: 09/011,151 BER: 09/011,151 BER: 09/011,151 BER: 09/011,151 BER: 09/011,143 BER: 09/11,143	
ttion US/09774 ing 20082677A1 ing 2008267 ing 200	100.0%; 100.0%; ative
UT 1 9-774-381-58 Buleance 58, Application US, Buleance 58, Application US, Bulcation No. US200300826, Bulcation No. US200300826, Bulcation No. US200300826, Bulcant: Holtzman, Doug PEPLICANT: Holtzman, Doug PEPLICANT: Ben, Yang PEPLICANT: Ben, Yang PELICANT: Gearing, David ITLE OF INVENTION: AND US URERY APPLICATION NUMBER: RIOR PILING DATE: 1998-0 RIOR PILING DATE: 1997-1 RIOR PELING DATE: 19	100 larity 100 Conservative
1-381-58 10: 58 A Publica 10: 58 A Publica 10: 10: 10: 10: 10: 10: 10: 10: 10: 10:	ch al Simi 303;
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                                LATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTGGQKSGFLRISNLQKQDQ 120
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1 MGRPLLLPLLPLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE 60
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Gorman, Daniel M.
McClanahan, Terrill K.
Zurawski, Sandra M.
Zurawski, Gerard
Lanter, Lewis L.
Phillips Jor., Joseph H.
TITLE OF INVENTION: Isolated Mammalian Monocyte Cell Genes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Palo Alto
CITY: Palo Alto
COMPUTER: California
COMPUTER READABLE FORM:
MEDIUM TYPE: Riopy disk
COMPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PRING DATE: 08-No. US20030105303A-2002
CLASSIFICATION: OWNER: US/10/290, 631
FILING DATE: 08-No. US20030105303A-2002
CLASSIFICATION: AUNENCE: US/08/985,950
PRING APPLICATION NUMBER: US/08/985,950
PILING DATE: 12-MARCH-1997
APPLICATION NUMBER: US 60/041,279
FILING DATE: 11-MARCH-1997
APPLICATION NUMBER: US 60/033,181
FILING DATE: 16-DEC-1996
APPLICATION NUMBER: US 60/032,252
FILING DATE: 16-DEC-1996
APPLICATION NUMBER: US 60/032,252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
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REGISTRATION NUMBER: 34,090
REPERENCE/DOCKET NUMBER: DX0670K
TELECOMMUNICATION INFORMATION:
TELEPRAX: (650)496-1204
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/10290631
Publication No. US20030105303A1
GENERAL INFORMATION:
APPLICANT: Adema, Gosse Jan
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Sequence 2, Application US/10780043

Sequence 2, Application US/10780043

Publication No. US20040137506A1

GENERAL INFORMATION:

APPLICANT: Bates, Elizabeth

APPLICANT: Bates, Lionel

APPLICANT: Chalus, Lionel

APPLICANT: Grarrone, Pierre

TITLE OF INVENTION: MONOCYTE-DERIVED NUCLEIC ACIDS AND RELATED COMPOSITIONS AND METHOI

FILE REFERENCE: SF0977X

CURRENT APPLICATION NUMBER: US/09/869,388

FILE REPARENCATION NUMBER: US/09/869,388

PRIOR FILING DATE: 2002-02-17

PRIOR FILING DATE: 2002-02-21

SQFTWARE: IBM PC compatible

SQFTWARE: IBM PC compatible

SQFTWARE: IBM PC compatible

SEQ ID NO 2

LENGTH: 303
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Pred. No. 6.6e-126;
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                           TYPE: emino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
LENGTH: 303 amino acids
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Matches 303; Conservative
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ORGANISM: homo sapiens
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December 23, 2005, 20:41:30 ; Search time 5.7416 Seconds (without alignments) 376.418 Million cell updates/sec
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1: /cgn2 6/ptodata/2/pubpaa/US08 NEW PUB.pep:*

2: /cgn2 6/ptodata/2/pubpaa/US06 NEW PUB.pep:*

3: /cgn2 6/ptodata/2/pubpaa/US07 NEW PUB.pep:*

4: /cgn2 6/ptodata/2/pubpaa/DS07 NEW PUB.pep:*

5: /cgn2 6/ptodata/2/pubpaa/US10 NEW PUB.pep:*

7: /cgn2 6/ptodata/2/pubpaa/US10 NEW PUB.pep:*

7: /cgn2 6/ptodata/2/pubpaa/US10 NEW PUB.pep:*

8: /cgn2 6/ptodata/2/pubpaa/US10 NEW PUB.pep:*

8: /cgn2 6/ptodata/2/pubpaa/US10 NEW PUB.pep:*
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-11-054-515-1841
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Maximum Match 100%
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	104	Seguence	US-11-054-515-1046	7	251	6.3	100	41
	156	Sequence	US-11-054-515-1561	7	. 250	6.3	100	40
0, Ap		Sequence	US-11-054-515-2080	7	256	6.3	100.5	39
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, App		Sequence	US-11-054-515-540	7	249	6.3	100.5	37
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1, Ap	1021	Sequence	US-11-054-515-1021	7	252	6.4	102.5	53
7, Ap	3247	Seguence	US-11-054-515-3247	-	250	6.4	102.5	28
7, Ap	1827	Seguence	US-11-054-515-1827	7	251	6.5	103	27
2096, Ap			0004-040-800-41-00		747	6.5	103	97

ALIGNMENTS

Sequence 391, Application US/11000463
| Sequence 391, Application US/11000463
| Publication No. US20050266423A1
| GENERAL INFORMATION:
| APPLICANT: Tang, Y Tom
| APPLICANT: Chen, Rul-hong
| APPLICANT: Chen, Rul-hong B. APPLICANT: Wang, Zhiwei
| APPLICANT: Chen, Ping
| PRIOR PILING DATE: 2001-01-25
| PRIOR PILING DATE: 2001-01-25
| PRIOR PILING DATE: 2000-01-17
| PRIOR PILING DATE: 2000-01-17
| PRIOR PILING DATE: 2000-01-17
| PRIOR PILING DATE: 2000-09-15
| P

Query Match 9.3%; Score 148.5; DB 7; Length 305; Best Local Similarity 23.5%; Pred. No. 5.1e-06; Matches 80; Conservative 52; Mismatches 125; Indels 83; Gaps

7 LPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWELATAPD

8

16; 66

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---WWCRGAIWRDCKILVKTSGSEQE-VKRDRVSIKDNQKNRTFTVTWEDLMKTDADTYW 107
                                                                                                                                                          65 PD-VRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQ------KSGFLRISN 114
                                                                                                                     125 CRVELDTRSSGROOMQSIEGTKLSITQAVT---TTTQRPSSMTTTW------RLSSTT 173
                                                                                                                                                                                                                                        174 TTTGLRVTQGKRRSDSWHISLETAVGVAVAVTVLGIMILGLICLLRWRRRKGQQRTKATT 233
                                                                                                                                                                                                                                                                                                                                                             234 PAR--EPPONTEEPYENIRNEGONTDP----KLN-------PKDDGIVY 269
   67 VRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRIS--NLQKQDQSVYF 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LILILILPLIAGTKGMR--GDRQYGDGYLLQVQE--LVTVQEGLCVHVPCSF8YPQDGWTD 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 LLLPLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWELATA 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 7.6%; Score 121; DB 7; Length 406; Best Local Similarity 24.7%; Pred. No. 0.0017; Matches 74; Conservative 37; Mismatches 130; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Lulu, Chengnua
APPLICANT: Chen, Willood
APPLICANT: Chen, Willood
APPLICANT: Chen, Xiachong B.
APPLICANT: Wentwell
APPLICANT: Wentwell
APPLICANT: Wentwell
APPLICANT: Wentwell
APPLICANT: Shou, Ping
APPLICANT: Zhou, Ping
APPLICANT: Cao, Yi-Cheng
APPLICANT: Chou, Yi-Cheng
APPLICANT: Chou, Yi-Cheng
APPLICANT: Chou, Ping
APPLICANT: Cao, Yi-Cheng
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: NOVel Nucleic Acids and Polypeptides
FILE REFERENCE: 785CIP4CN
CURRENT PILING DATE: 2004-11-29
FRIOR APPLICATION NUMBER: 10/291,265
FRIOR PILING DATE: 2001-01-25
FRIOR APPLICATION NUMBER: 09/491,404
FRIOR APPLICATION NUMBER: 09/491,404
FRIOR APPLICATION NUMBER: 09/491,404
FRIOR PILING DATE: 2000-01-15
FRIOR APPLICATION NUMBER: 09/611,71
FRIOR PILING DATE: 2000-01-25
FRIOR PILING DATE: 2000-01-25
FRIOR APPLICATION NUMBER: 09/631,451
FRIOR APPLICATION NUMBER: 09/631,451
FRIOR APPLICATION NUMBER: 09/631,451
FRIOR PILING DATE: 2000-09-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        270 ASLALSSSTSPRAP-----PSHRPLKSPQNETLYSVL 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 377, Application US/11000463
Publication No. US20050266423A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tang, Y Tom
Liu, Chenghua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -11-000-463-377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-11-000-463-377
                                                             22
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                                                                                                                                                                                                                  TTTGLRVTQGKRRSDSWHISLETAVGVAVAVTVLGIMILGLICLLRWRRKKGQQRTKATT 233
                                                                                                                                                                                                                                                                                                                                  PAR--EPPQNTEEPYENIRNEGONTDP----KLN-------PKDDGIVY 269
                                                                                                ---WWCRGAIWRDCKILVKTSGSEQE-VKRDRVSIKDNQKNRTFTVTWEDLMKTDADTYW 107
                                                                                                                                                                             CRVELDTRSSGROOMQSIEGTKLSITQAVT---TTTQRPSSMTTTW------RLSSTT 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          207 PROVLOPLEG-DLCYADLTLQLAGISPRKATTKLSSAQVDQVEVEYVTMASLPKED-ISY 264
                                                       67 VRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRIS--NLQKQDQSVYF 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 LPLLLPLLLPPAFLQPSGSTGSGPSYLYGVTQPXHLSASMGGSVEIPFSFYYPWELATAPD 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MPLLTLYLLLFWL-----SGYSIVTQITGPTTVNGLERGSLTVQCVYRSGWETYLK-- 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 7; Length 305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Tang, Y Tom
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Chen, Kischong B.
APPLICANT: Wehrman, Tom
APPLICANT: Anng, Zhiwei
APPLICANT: Zhou, Ping
APPLICANT: Zhou, Ping
APPLICANT: Zhou, Ping
APPLICANT: Zhou, Ping
APPLICANT: Cao, Yi-Cheng
APPLICANT: Drawnac, Radoje T.
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 785CIP4CN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   265 ASLILGA--EDQEPTYCNMGHLSSHLPGRGPEEPTEYSTI 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           270 ASLALSSSTSPRAP-----PSHRPLKSPQNETLYSVL 301
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9.2%; Score 146.5; DB 7;
Best Local Similarity 23.5%; Pred. No. 7.6e-06;
Matches 80; Conservative 51; Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT FILING DATE: 2004-11-29

PRIOR APPLICATION NUMBER: 10/291,265

PRIOR FILING DATE: 2002-11-08

PRIOR FILING DATE: 2001-10-25

PRIOR FILING DATE: 2001-01-25

PRIOR FILING DATE: 2001-01-25

PRIOR FILING DATE: 2001-08-03

PRIOR FILING DATE: 2000-01-25

PRIOR FILING DATE: 2000-01-3

PRIOR FILING DATE: 2000-08-03

PRIOR FILING DATE: 2000-08-03

PRIOR FILING DATE: 2000-08-03

PRIOR FILING DATE: 2000-08-03

PRIOR FILING DATE: 2000-09-15

NUMBER OF SEQ ID NOS: 944

SOFTWARE: FREUSEQ for Windows Version 3.0

SEQ ID NO 863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/11/000,463 CURRENT FILING DATE: 2004-11-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 863, Application US/11000463
Publication No. US20050266423A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) ORGANISM: Homo sapiens
US-11-000-463-863
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                                                                                                                                                                                                                                                                                                                                                                                                                  234
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13;

GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

December 23, 2005, 20:20:08; Search time 21.1395 Seconds (without alignments) 1379:107 Million cell updates/sec

Title: Perfect score: Sequence:

US-10-780-043-2 1591 1 MGRPLLLPLLPLLLPPAFLQ......PSHRPLKSPQNETLYSVLKA 303

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seg length: 0 Maximum DB seg length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 80:*
1: pirl:*
2: pir2:*
3: pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES	
Result No.	Score	Query Match	Length	DB		escripti
-	144.5	9.1	823	7	S48394	probable membrane
7	123.5	7.8	1114	7	T49517	p63 related protei
٣	118.5	7.4	509	~	JC5288	SHP substrate-1 pr
4	116	7.3	392	7	B44194	poliovirus recepto
S	116	7.3	417	7	A44194	poliovirus recepto
9	115.5	7.3	513	7	JC5289	SHP substrate-1 pr
7	114	7.2	392	-	RWHUPD	poliovirus recepto
c o	114	7.2	417	н	RWHUPA	poliovirus recepto
6	112.5	7.1	403	7	152590	
10	110	6.9	235	~	825758	Iq lambda chain -
11	110	•	847	~	JH0371	B-cell adhesion pr
12	109.5		233	~	S25747	lambda chain
13	108.5	•	230	7	S49449	
14	108.5	6.8	235	7	S14675	Ig lambda chain -
15	108.5	6.8	862	~	149583	differentiation an
16	108.5		868	~	A46512	CD22 homolog/B lym
17	108		236	7	S25746	Ig lambda chain -
18	108	6.8	1694	7	850065	Bialoadhesin - mou
19	106	6.7	647	~	A35648	B-cell adhesion pr
50	106		710	~	A99486	ABC transporter, b
21	105.5		235	7	S25750	Ig lambda chain -
22	104.5	•	214	ď	PC4156	Ig lambda chain V
23	104	6.5	231	~	825751	Ig lambda chain -
24	104	•	798	~	T34248	
25	103	6.5	446	~	T45525	WSC4 homolog [impo
56	103	6.5	469	~	S37483	ΰ
27	102.5	6.4	407	7	T08732	
28	102	6.4	572	7	B46529	
59	101	6.3	118	7	E27889	Ig heavy chain V r

hypothetical prote rearranged T-cell	Ig heavy chain pre MHC class I histoc All 2 - human	MHC class I histoc hypothetical prote	T-cell surrace gly Ig lambda chain - Ig lambda chain -	Ig lambda chain NI Ig lambda chain - VpreB protein prec	Ig kappa chain pre MHC class I protei neurofascin – chic
T34293 I46626	B26471 A47636 T83063	137478 T04520	S25657 S25738 S25756	JE0246 S25759 A28344	A20969 I36961 S26180
20	0 0 0	000	7 7 7	000	000
790	152 365 365	365 413	231 231 232	217 235 142	229 365 1272
6.3	999		9 9 9	6 6 6 6 6 6 6 6 6	6.1
101	100.5	100	5 5 5 5 5 5	9 9 9 9 8 8 7	97 97 97
30	33.2	999	37 38 39	4 4 4 0 1 2	4 4 4 5 4 5

ALIGNMENTS

RESULT 1 S48394	
probable C;Species C;Date: (probable membrane protein Ylui40w - yeast (Saccharomyces cerevisiae) C;Species: Saccharomyces cerevisiae C;Date: 02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 09-Jul-2004 C:Accesion: &48144. &560776
R; Churcher,	5r, C. 1 to the RMBL Data Library, Sentember 1994
A; Referer A; Accessi	A, Reference number: \$48310
A; Molecul	A; Molecule type: DNA A. Regidnes: 1-823 <chi></chi>
A, Cross-1	A;Cross-references; UNIPROT: P38928; UNIPARC: UPI000012669C; GB:Z47047; EMBL: Z38059; NID:9
R; Torpey, Yeast 10.	R;Torpey, L.E.; Gibbs, P.E.M.; Nelson, J.; Lawrence, C.W. Yeast 10, 1503-1509, 1994
A, Title:	Cloning and sequence of RBV7, a gene whose function is required for DNA damage-
A; Accessi	A;Kererence number: S502/5; MUID:951/6/09; FMID:/6/1890 A;Accession: S50276
A, Statue	A; Status: nucleic acid sequence not shown; translation not shown
A; Molecul	A;MOLECULE Type: DNA A:Residues: 80-823 <tor></tor>
A;Cross-1	A;Cross-references: UNIPARC:UPI00001689D0; EMBL:U07228; NID:9460247; PIDN:AAA67919.1; PI A:Note: the nucleotide sequence was submitted to the EMBL Data Library. March 1994
C;Genetics:	183
A; Cross-1	A;Cross-references: SGD:S0001402; MIPS:YIL140w
A; Map position: C; Superfamily: S	A;Map position: 9L C;Superfamily: Saccharomyces cerevisiae probable membrane protein YIL140w
C; Keyword F; 6-22/DC F; 511-527	C:Keywords: transmembrane protein F:6-12/Domain: transmembrane #status predicted <tmi> F:511-577/Domain: transmembrane #status predicted <tm2></tm2></tmi>
	March 9 1% Score 144 5 DR 2 Length 823.
Best Lo Matcher	Best Local Similarity 24.7%; Fred. No. 0.0024; Matches 72; Conservative 45; Mismatches 96; Indels 79; Gaps 16;
È	25 TGSGPSYLYGV-TQPKHLSASMGGSVEIPPSFYYPWELATAPDVRISWRR 73
QQ	308 SGSVPDELLGKNSNPANFSVSIYDTYGDVIYFNFRVVSTTDLFAISSLPNINATR 362
ò	74 GHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRIS 113
d d	363 GEWFSYYFLPSQFTDYVNTNVSLEFTNSSQDHDWVKFQSSNLTLAGEVPKNFDKLS 418
ò	114NLOKODQSVYFCRVELDTRSSGRQQWQSIBGTKLSITQAVTTTTQRPSSMTTTWR 168
qq	419 'LGLKANGGSQSQELYFNIIGMDSKITHSNHSANATSTRSSHHSTSTSSYTSSTYTAK 475
ò	169 LSSTTTITGLRVTQGKRRSDSWHISLETAVGVAVAVTV-LGIMILGLIC-LLRWRRR 223
qq	476 ISSTSABALSSAPAALPAANKTSSHNKKAVALACGVALPLGVILVALICPLIFWRRR 532

13;

65; Gaps

175

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C;Accession: B4194
R;Koike, S:; 18e, I.; Sato, Y.; Yonekawa, H.; Gotoh, O.; Nomoto, A.
Virol. 66, 7059-7066, 1992
A;Title: A second gene for the African green monkey poliovirus receptor that has no puta A;Reference number: A44194; MUID:93059651; PMID:1331508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 APDVRISWRRGHFHGQS-----FYSTRPPSIHKDYVNRLFLNWTEGQKSGF------ 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HVS-QLTWSR---HGESGSMAVFHQTQGP------NYSEPKRLBFVARLGTEL 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         110 ---- LRISNLOKODOSVYRC------RVELDTRSSGROOWOSIEGTKLSI 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       150 TQAVTTTTQRPSSMTTTWR----- 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------YPPEVSISGYD 252
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                                                                                                                                                                                                                                                                                                                                                                                                             176 TGLRVTQGKRRSDSWHISLETAVGVAVAVTVLGIMILGLICLLRWRRKKGQQRTKATTPA 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                164 ARCVSTGGRPPAHI -- TWHSDLGGMPNTSQAPGFLSGTVTVTSLWILVPSSQVDGKSVTC 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N----IRNEGONT-DPKLNPKDDGIVYASLALSSSTSPRAPPSH------RPLKSPQ 293
                                                                                                                                                                                                                                                             279 FYP-----EDLOLIWLE---NGNVSRNDTPKNLTKN-----TDGTYNYTSLFLVNSSA 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               236 REPFQNTEEPYENIRNEGQNTDPKLNPKDDGIVYASLAL--SSSTSPRAPPSHRPLKSPQ 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        poliovirus receptor (clone AGM-delta-1) - green monkey
C;Species: Cercopithecus aethiops (green monkey, grivet)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --WHISLETAVGVAVAVTVLGIMILGLICLLRWRRRKGQQRTKATTPAREPFQNTEEPYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLILILIELSWPP-----PGTGDII----VQAPTQVPGFLGDSVTLPCYLQVPGMEET
                                                                                                                                                                                                                                                                                                                                                             116 QKQDQSVYFCRVELDTRSSGRQQWQSIEGTKLSITQAVTTTTQRPSSMTTTWRLSSTTTT
                                                                                                                                                                       56 YYPWELATAPDVRISWRRGHFHGQSFYSTRPPSIHKDYVNRLFLNWTEGQKSGFLRISNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 PLLLPLLPLLPPAFLQPSGSTGSGPSYLYGVTQPKHLSASMGGSVBIPFSFYYPWELAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 7.3%; Score 116; DB 2; Length 392; Best Local Similarity 21.2%; Pred. No. 0.15; Matches 77; Conservative 42; Mismatches 110; Indels 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GB: S48817
                                                                            Indels
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. 0.14;
                            Similarity 22.9%; Pred. No. 0.14; 57; Conservative 44; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      222 KVEHESFEKPQLLTVNLTVY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     294 NETLYSVLK 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | | |: ::
NHTEYASIE 464
                   Best Local Similarity
Matches 57; Conserv
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SUCTORE
SHE SUbstrate-1 protein, 509 - mouse
SHE substrate-1 protein, 509 - mouse
CiSpecies: Mus musculus (house mouse)
CiSpecies: Mus musculus (house mouse)
CiSpecies: Musculus (house mouse)
CiDate: 16-Apr-1997 #sequence_revision 09-May-1997 #text_change 20-Jun-2000
CiAccession: JC5288
Rivamaco, T.; Matcaaki, T.; Amano, K.; Matsuda, Y.; Takahashi, N.; Ochi, F.; Fujioka, Y.;
Biochem: Biophys. Res. Commun. 231, 61-67, 1997
Alfitle: Mouse and human SHPS-1: Molecular cloning of cDNAs and chromosomal localization A, Reference number: JC5287; MuID:97223399; PMID:9070220
A, Contents: Brain
A, Accession: JC5288
A, Molecula type: mRNA
A, Residuale type: mRNA
A, Contents: 1-500 extANA
A, Conte
                                                                                                                                                                                                                                                                                                                                p63 related protein [imported] - Neurospora crassa
N/Alternate names: protein B14D6.690
C/Species: Neurospora crassa
A/Reference number: Z2502
A/Reference number: Z2502
A/Residues: Z2502
A/Residues: DA
A/Residues: 1-1114 < SCH>
A/Residues: 1-1114 < SCH>
A/Residues: 1-1114 < SCH>
A/Residues: 1-1114 SCH>
A/Residues: 1-1144 SCH>
A/Residues: 1-1444 SCH>
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A/Residues: 
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C;Comment: This protein is a glycosylated receptor-like protein and plays a role in cell
acts as a docking protein and induce translocation of SHP-2 from the cytosol to the pla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               155 GSDPADL-----ATMTISDDKDFMFY-----APLIQINWQS-----SDR 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86 PPSIHKDYVNRLFLNWTEGQKSGFLRISNLQKQDQSVYFCRVELDTRSSGRQQWQSIEGT 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-----VDVDTMST----LAT 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AVTVLGIMILGLICLLRWRRRKGQQR-----TKATTPAREPFQNTE----- 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       271 AGGVLAVAIVAIIFICAWRRRKQQMEEBEPDRMYGMKDVGPSTADFRNEEIPGWHRGPTR 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWELATAPDVRISWRRGHFHGQSFYSTR 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                  533 RENPODENLPHAISGPDLNNPANKPNO------ENATPLNNPPDD 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81; Indels 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 1114;
                                 224 KGQQRTK------ATTPAREPFQNTEEPYENIRNEGQNTDPKLNPKDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                331 RQPPAPVDPFRSDGES------ELMAPPAPYHPPS 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----EPYENIRNEGONTDPKLNPKDDGIVYASLALSSSTSPRAPPS 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 7.8%; Score 123.5; DB Best Local Similarity 23.1%; Pred. No. 0.14; Matches 66; Conservative 32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: NCSP:B14D6.690
A;Map position: 6
A;Introns: 132/2; 362/2; 427/3; 540/3
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247

307 NTT 309

DB 2; Length 509;

7.4%; Score 118.5;

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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: December 23, 2005, 20:19:13 ; Search time 130.752 Seconds

(without alignments)

1634.967 Million cell updates/sec
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1634.967 Million cell updates/
Title: US-10-780-043-2
Perfect score: 1591
Sequence: 1 MGRPLLLPPLLPPAFLQ......PSHRPLKSPQNETLYSVLKA 303

Sequence: 1 MGRPLLLPLLPLLPPAFT Scoring table: BLOSUM62

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 2166443 Beqg, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : Uniprot_05.80:* 1: uniprot_sprot:* 2: uniprot_trembl:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	homod	Q8nhil homo sapien	Q9ukjo homo sapien	Q8bya6 mus musculu	P38928 saccharomyc	Q6ux24 homo sapien	Q7z6a6 homo sapien	homo	homo	Q9nyz4 homo sapien	mus m	Q8tbc9 homo sapien	Q5dwn6 eptatretus		Q7sdq5 neurospora	Q5tyt7 brachydanio	Q99m11 mus musculu	046707 fugu rubrip	Q9gje4 fugu rubrip		Q5w433 brachydanio	Q6piq7 homo sapien	Q5dwn5 eptatretus	Q872v2 neurospora	Q91b03 sphoeroides	Q6p2j1 homo sapien		P32506 cercopithec	_	fugn	Q6pjg0 homo sapien
SUMMAKIES		CI.	Q9UKJ1 HUMAN	Q8NHI1 HUMAN	Q9UKJ0 HUMAN	Q8BYA6 MOUSE	AXL2 YEAST	Q6UX24 HUMAN	Q7Z6A6_HUMAN	Q8TDQ1_HUMAN	Q7Z7I5 HUMAN	SIGL8 HUMAN	Q6QX36 MOUSE	Q8TBC9 HUMAN	QSDWN6_EPTBU	Q6ZMC9_HUMAN	Q7SDQ5_NEUCR	QSTYT7_BRARE	Q99M11 MOUSE	O46707 FUGRU	Q9GJE4_FUGRU	Q5W434_BRARE	Q5W433_BRARE	O6PIQ7 HUMAN	Q5DWNS_EPTBU	Q872V2 NEUCR	Q9IB03 9PERC	Q6P2J1_HUMAN	O46705_FUGRU	PVR CERAE	SHPS1_MOUSE	046706_FUGRU	Q6PJG0 HUMAN
		80	~	~	~	~	Н	N	7	~	~	H	N	~	7	~	7	N	~	7	N	0	~	~	N	~	~	~	~	н	-	7	~
		Match Length DB	303	226	227	299	823	290	290	290	293	499	289	233	283	328	353	828	235	288	367	633	651	236	283	434	318	235		417		367	235
d	Query	Match	99.8	62.7	60.2	39.6	9.1	8.7	8.7	8.5	8.5	8.2	8.2	8.1	8.0	7.8	7.8	7.8	7.7	7.7	7.7	7.6	7.6	7.5	7.5	7.5	7.5	7.4	7.4	7.3	7.3	7.2	7.2
		Score	1588	997.5	958	630	144.5	139	139	136	135.5	130.5	130	129.5	127	123.5	123.5	123.5	122.5	122	122	121.5	121.5	120	120	119.5	119	117.5	117.5	116	115.5	115	114.5
	Result	No.	п	Α,	٣	4	S	9	7	æ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31

Q5dwn4 eptatretus Q96ap7 homo sapien P15151 homo sapien Q99795 homo sapien O5vzo6 homo sapien	064ja4 pan troglod 05dwn2 eptatretus 008835 cercopithec 073675 xenopus lae	Q6pck4 xenopus lae Q63994 mus musculu Q8tgO0 aspergillus Q4w889 aspergillus O76894 drosophila
QSDWN4 EPTBU ESAM HUMAN PVR HUMAN GPA33 HUMAN OSVZPE HUMAN	SIG13 PANTR Q5DWNZ EPTBU Q08835 CERAE O73675 XENLA	Q6PCK4_XENLA CD33 MÖUSB Q8TGGO ASPFU Q4WS89_ASPFU O76894_DROME
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ALIGNMENTS

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SVYFCRVELDTRSSGROOMQSIEGTKLSITOAVTTTTORPSSMTTTWRLSSTTTTTGLRV 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IntAct; Q9UKJO; -. Goldens of the colors of the color of the col
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Pouetka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
Mewes H.W., Well B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MGRPLILPILPILDIQPPAFLQPGGSTGSGPSYLYGVTQPKHLSASMGGSVEIPFSFYYPWE
                                                                                                                                  181 TQGKRRSDSWHISLETAVGVAVAVTVLGIMILGLICLLRWRRRKGQQRTKATTPAREPFQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-FRAZ-2005 (TrEMBLrel. 29, Last annotation update)
Activating receptor Pilkbeta (Hypothetical protein DKFZp4340079)
Name=DKFZp4340079;
                                                                                                                                                                                                                                                                                                                    241 NTEEPYENIRNEGONTOPKINPKODGIVYASLALSSSTSPRAPPSHRPL 289
                                                                                                                                                                                                                                                                                                                                                                       168 NTEEPYENIRNEGONTDPKLNPK----LHLTQSTSQPPSPQEPPERDPV 212
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60.2%; Score 958; DB 2; Length 227;
Best Local Similarity 80.8%; Pred. No. 1.7e-71;
Matches 185; Conservative 15; Mismatches 19; Indels 1
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EMBL; AF161081; AAD52965.1; -; mRNA.
EMBL; AL834336; CAH10711.1; -; mRNA.
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Hypothetical protein; Immunoglobulin domain; Receptor.
SEQUENCE 227 AA; 25542 MW; 7FF960C60AB7EF09 CRC64;
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InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OFUKJO HUMAN PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
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Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bate N.K.,
Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bate N.K.,
Altschul R.P., Jordan H., Moore T., Max S.I., Wang J., Haidh F.,
Blatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brownstein M., Soares M.B., Bonaldo M.F., Carainci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Boosak S.A., McKernan K.J., Malek J.A., Gunzatne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gabb B.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.B.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.B.,
B. Monstan D.N., Marzywinski M.I., Skalska U., Smailus D.B.,
B. Maria D.N., Marzywinski M.I., Skalska U., Smailus D.B.,
B. Maria D.N., Marzywinski M.I., Skalska U., Smailus D.B.,
B. Maria D.N., Marzywinski M.I., Skalska U., Smailus D.B.,
B. Maria D.N., Marzywinski M.I., Skalska U., Smailus D.B.,
B. Maria D.N., Marzywinski M.I., Skalska U., Smailus D.B.,
B. Maria D.N., Marzywinski M.I., Skalska U., Smailus D.B.,
B. Maria D.N., Marzywinski M.I., Skalska U., Smailus D.B.,
B. Maria D.N., Marzywinski M.I., Skalska U., Smailus D.B.,
B. Maria D.N., Marzywinski M.I., Skalska U., Smailus D.B.,
B. Maria D.N., Marzywinski M.I., Skalska U., Smailus D.B.,
B. Maria D.N., Marzywinski M.I., Skalska U., Smailus D.B.,
B. Maria D.N., Marzywinski M.I., Skalska U., Smailus D.B.,
B. Maria D.N., Marzywinski M.I., Skalska U., Smailus D.B.,
B. Maria D.N., Marzywinski M.I., Skalska U., Smailus D.B.,
B. Maria D.N., Marzywinski M.I., Skalska U., Smailus D.B.,
B. Maria D.N., Marzywinski M.I., Skalska U., Smailus D.B.,
B. Maria M. W. Shalska U., Smailus D.B.,
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                                              300
                                                                                             241 NTEEPYENIRNEGONTDPKLNPKDDGIVYASLALSSSTSPKAPPSHRPLKSPONETLYSV 300
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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Pred. No. 8.7e-75;
6; Mismatches 10; Indels 77;
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Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC017812; AAH17012.1; -; mRNA.
InterPro; IPR003599; Ig.
InterPro; IPR001110; Ig-11ke.
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Immunoglobulin domain.
SEQUENCE 226 Aa; 25479 MW; 5938181797733A30 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation update)
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ilarity 67.8%;
Conservative
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01-OCT-2002 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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